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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 165 Seconds  
(without alignments)  
309.408 Million cell updates/sec

Title: US-10-643-836-297  
Perfect score: 703  
Sequence: 1 MEGGAYAGKAGGAFDPYTL.....GEPHPAGTCTSTEGCPGP 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Genesecp1980s:\*

2: Genesecp1990s:\*

3: Genesecp2000s:\*

4: Genesecp2001s:\*

5: Genesecp2002s:\*

6: Genesecp2003as:\*

7: Genesecp2003bs:\*

8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	703	100.0	132	4	AAG89177	Aag89177 Human sec
2	582.5	82.9	191	8	ABM84393	Abm84393 Human dia
3	577	82.1	112	3	AG00298	Ag00298 Human sec
4	577	82.1	191	4	AAM39280	Aam39280 Human pol
5	577	82.1	211	8	ABM84391	Abm84391 Human dia
6	415.5	59.1	210	4	AAM41065	Aam41065 Human pol
7	415.5	59.1	210	4	AAM41066	Aam41066 Human pol
8	415.5	59.1	210	4	AAM41067	Aam41067 Human pol
9	413	58.7	192	4	AAM39281	Aam39281 Human pol
10	403.5	57.4	192	4	AAM39279	Aam39279 Human pol
11	403.5	57.4	234	8	ABM84392	Abm84392 Human dia
12	403	57.3	217	4	ABG26417	Abg26417 Novel hum
13	353	50.2	229	8	ADO19528	Ado19528 Human PRO
14	350.5	49.9	212	8	ABM84066	Abm84066 Human dia
15	305.5	43.5	225	8	ADP04527	Adp04527 Sea squir
16	296	42.1	204	8	ADM72128	Adm72128 Human NTR
17	296	42.1	224	2	AAW36516	Aaw36516 Human syn
18	296	42.1	224	2	AAW36516	Aaw36516 Human syn
19	296	42.1	224	3	AAB44265	Aab44265 Human PRO
20	296	42.1	224	3	AAB24048	Aab24048 Human PRO
21	296	42.1	224	4	AAB64539	Aab64539 Gene 45 h
22	296	42.1	224	4	AAB64466	Aab64466 Human sec
23	296	42.1	224	4	AAB64540	Aab64540 Human sec
24	296	42.1	224	6	ABO25211	Ab025211 Novel hum
25	296	42.1	224	6	ABU72217	Abu72217 Novel hum

26	296	42.1	224	6	ABU84897	Abu84897 Human sec
27	296	42.1	224	6	ABU61095	Abu61095 Human PRO
28	296	42.1	224	6	ABU80364	Abu80364 Human sec
29	296	42.1	224	6	ADA24701	Ada24701 Novel hum
30	296	42.1	224	6	ABO19666	Ab019666 Novel hum
31	296	42.1	224	6	ADA12362	Ada12362 Human sec
32	296	42.1	224	6	ABO19557	Ab019557 Novel hum
33	296	42.1	224	6	ADB73668	Adb73668 Human PRO
34	296	42.1	224	7	ADB76384	Adb76384 Human PRO
35	296	42.1	224	7	ADC43810	Adc43810 Human sec
36	296	42.1	224	7	ADC61570	Adc61570 Human sec
37	296	42.1	224	7	ADC63534	Adc63534 Human sec
38	296	42.1	224	7	ADC66634	Adc66634 Human sec
39	296	42.1	224	7	ADC68758	Adc68758 Human sec
40	296	42.1	224	7	ADC62818	Adc62818 Human sec
41	296	42.1	224	7	ADC67883	Adc67883 Human sec
42	296	42.1	224	7	ADC41203	Adc41203 Human sec
43	296	42.1	224	7	ADC67258	Adc67258 Human sec
44	296	42.1	224	7	ADC62194	Adc62194 Human sec
45	296	42.1	224	7	ADC41827	Adc41827 Human sec
46	296	42.1	224	7	ADD45142	Add45142 Human PRO
47	296	42.1	224	7	ADE54986	Ades4986 Human PRO
48	296	42.1	224	7	AD849196	Ade49196 Human sec
49	296	42.1	224	7	ADE35250	Ade35250 Human sec
50	296	42.1	224	7	ADE16364	Ade16364 Human sec

ALIGNMENTS

RESULT 1  
AAG89177  
ID AAG89177 standard; protein; 132 AA.

XX AAG89177;

DT 11-SEP-2001 (first entry)

DE Human secreted protein, SEQ ID NO: 297.

XX Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;  
KW GENSET.

XX Homo sapiens.

PN WO200142451-A2.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-IB001938.

XX 08-DEC-1999; 99US-0169629P.

XX 06-MAR-2000; 2000US-0187470P.

XX (GSET ) GENSET.

PI Dumas Malne Edwards J, Bougueleret L, Jobert S;

DR WPI; 2001-367870/38.

DR N-PSDB; AAH64780.

XX Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.

XX Claim 21; Page 828; 921pp; English.

XX The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's

CC genome that affect the activity of GENSET or by supplementing the  
 CC patients own production of GENSET polypeptides. Conversely, antisense  
 CC nucleic acid molecules may be administered to down regulate GENSET  
 CC expression by binding with the cells' own genes and preventing their  
 CC expression. The sense and antisense nucleic acids may also be used as DNA  
 CC probes in diagnostic assays to detect and quantitate the presence of  
 CC similar nucleic acid sequences in samples, and hence to determine which  
 CC patients may be in need of restorative therapy. The GENSET polypeptides  
 CC may be used as antigens in the production of antibodies and in assays to  
 CC identify modulators (agonists and antagonists) of GENSET polypeptide  
 CC expression and activity. The present sequence is a GENSET polypeptide of  
 CC the invention  
 CC  
 XX Sequence 132 AA;  
 SQ  
 Query Match 100.0%; Score 703; DB 4; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60  
 DB 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60  
 QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 120  
 DB 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 120  
 QY 121 PCTESTEGCGPG 132  
 DB 121 PCTESTEGCGPG 132  
 RESULT 2  
 ABM84393  
 ID ABM84393 standard; protein; 191 AA.  
 AC ABM84393;  
 XX  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4642.  
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
 KW Homo sapiens.  
 OS  
 XX WO2004023973-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 12-SEP-2003; 2003WO-US028227.  
 XX  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 PA (INCY-) INCYTE CORP.  
 XX  
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
 PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
 PI Feralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patury S, Shi X, Suarez CJ;  
 XX  
 DR WPI: 2004-329368/30.  
 DR N-PSDB; ACN43045.  
 XX  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.

XX Claim 27; Page; 190pp; English.  
 PS  
 CC The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorders, developmental disorders, or  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
 CC  
 XX Sequence 191 AA;  
 SQ  
 Query Match 82.9%; Score 582.5; DB 8; Length 191;  
 Best Local Similarity 84.9%; Pred. No. 5.5e-61;  
 Matches 118; Conservative 3; Mismatches 3; Indels 15; Gaps 3;  
 QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60  
 DB 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60  
 QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 113  
 DB 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 120  
 QY 114 EHPAGTCTESTEG-CPG 131  
 DB 121 QP-----TERRDGRSPG 132  
 RESULT 3  
 AAG00298  
 ID AAG00298 standard; protein; 112 AA.  
 AC AAG00298;  
 XX  
 DT 06-OCT-2000 (first entry)  
 DE Human secreted protein, SEQ ID NO: 4379.  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping.  
 OS Homo sapiens.  
 XX EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-00200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI: 2000-500381/45.  
 DR N-PSDB; AAC00304.  
 XX  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 PT

PS Claim 13; SEQ ID NO 4379; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of

CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were

CC prepared from total human RNAs or polyA+ RNAs derived from 30 different

CC tissues. EST sequences usually correspond mainly to the 3' untranslated

CC region (UTR) of the mRNA because they are often obtained from oligo-dT

CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA

CC sequences derived from the 5' ends of mRNAs and even in those cases where

CC longer cDNA sequences have been obtained, the full 5' UTR is rarely

CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can

CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs

CC are also used in diagnostic, forensic, gene therapy and chromosome

CC mapping procedures. They are used to obtain upstream regulatory sequences

CC and to design expression and secretion vectors

XX

SEQ Sequence 112 AA;

Query Match 82.1%; Score 577; DB 3; Length 112;

Best Local Similarity 99.1%; Pred. No. 1.3e-60;

Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAGFDPYTLVRQPHITLVRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60

DB 1 MEGGAYGAGKAGGAGFDPYTLVRQPHITLVRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60

QY 61 YNRNPNACSYGVAVGLAFITLCLLYLALDVYFQISSVKDKKAVLSIDIGVS 112

DB 61 YNRNPNACSYGVAVGLAFITLCLLYLALDVYFQISSVKDKKAVLSIDIGVS 112

RESULT 4

AM39280

ID AAM39280 standard; protein; 191 AA.

XX

AC AAM39280;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2425.

XX

KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US034263.

XX

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX

PA (HYSEQ-) HYSEQ INC.

XX

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX

XX WPI; 2001-442253/47.

DR N-PSDB; AAI58436.

XX

PT Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.

XX

PS Example 4; SEQ ID NO 2425; 10078pp; English.

XX

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemia and

CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification

XX

SEQ Sequence 191 AA;

Query Match 82.1%; Score 577; DB 4; Length 191;

Best Local Similarity 99.1%; Pred. No. 2.5e-60;

Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAGFDPYTLVRQPHITLVRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60

DB 1 MEGGAYGAGKAGGAGFDPYTLVRQPHITLVRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60

QY 61 YNRNPNACSYGVAVGLAFITLCLLYLALDVYFQISSVKDKKAVLSIDIGVS 112

DB 61 YNRNPNACSYGVAVGLAFITLCLLYLALDVYFQISSVKDKKAVLSIDIGVS 112

RESULT 5

ABM84391

ID ABM84391 standard; protein; 211 AA.

XX

AC ABM84391;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4640.

XX

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX

OS Homo sapiens.

XX

PN WO2004023973-A2.

XX

PD 25-MAR-2004.

XX

PF 12-SEP-2003; 2003WO-US028227.

XX

PR 12-SEP-2002; 2002US-04102599.

PR 12-SEP-2002; 2002US-0410260P.

XX

PA (INCY-) INCYTE CORP.

XX

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kitton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JB, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX

XX WPI; 2004-329368/30.

DR N-PSDB; ACN43043.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorder, endocrine

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dithp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dithp protein of the

CC invention. Note: The sequence data for this patent is not represented in

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 211 AA;

SQ

Query Match 82.1%; Score 577; DB 8; Length 211;

Best Local Similarity 99.1%; Pred. No. 2.8e-60;

Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNNGYLNSASEGEQFCI 60

DB 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNNGYLNSASEGEFCI 60

QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDIGVS 112

DB 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDIGVS 112

RESULT 6

AAM41065

ID AAM41065 standard; protein; 210 AA.

XX AAM41065;

AC AAM41065;

XX 22-OCT-2001 (first entry)

DT Human polypeptide SEQ ID NO 5996.

DE

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX Homo sapiens.

OS

XX WO200153312-A1.

PN

XX 26-JUL-2001.

PD

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00489725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI60221.

XX Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.

XX Example 2; SEQ ID NO 5996; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as; Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification

XX Sequence 210 AA;

SQ

Query Match 59.1%; Score 415.5; DB 4; Length 210;

Best Local Similarity 66.4%; Pred. No. 5.9e-41;

Matches 89; Conservative 2; Mismatches 10; Indels 33; Gaps 3;

QY 31 VSW-----LFSIVVFGSIVNNGYLNSASEGEQFCIYNRNPACSYGVAVGVLAFLTCL 83

DB 34 VSWRSRPGCELFSIVVFGSIVNNGYLNSASEGEFCIYNRNPACSYGVAVGVLAFLTCL 93

QY 84 LYLALDVYFPQISSVKDRKAVLSDIG-VSGPHPAG----- 119

DB 94 LYLALDVYFPQISSVKDRKAVLSGHVVSVEGHPAPFAFWLFTGDCSYLANQWQVSKP 153

QY 120 --TPCTESTGCPG 131

DB 154 KDNPLNEGTDASPG 167

RESULT 7

AAM41066

ID AAM41066 standard; protein; 210 AA.

XX AAM41066;

AC AAM41066;

XX 22-OCT-2001 (first entry)

DT Human polypeptide SEQ ID NO 5997.

DE

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX Homo sapiens.

OS

XX WO200153312-A1.

PN

XX



Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 13-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AA160223.

XX Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

PT Example 2; SEQ ID NO 5998; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA157798-AA161369) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

XX Sequence 210 AA;

Query Match 59.1%; Score 415.5; DB 4; Length 210;

Best Local Similarity 66.4%; Pred. No. 5.9e-41;

Matches 89; Conservative 2; Mismatches 10; Indels 33; Gaps 3;

QY 31 VSW-----LFSIVVFGSIWNEGYLNSASEGQFCIYNRPNACSYGVAVGLAFLTCL 83

DB 34 VSWRSRPGCELFSIWVFGSIWNEGYLNSASEGQFCIYNRPNACSYGVAVGLAFLTCL 93

QY 84 LYALDVFYFQISSVKDRKXAVLSDIG-VSGEHPAG----- 119

DB 94 LYALDVFYFQISSVKDRKXAVLSDIG-VSGEHPAG----- 119

QY 120 --TFCTESTEGCGP 131

DB 154 KDNPLNEGTDASPG 167

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 13-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AA160222.

XX Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

PT Example 2; SEQ ID NO 5997; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA157798-AA161369) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

XX Sequence 210 AA;

Query Match 59.1%; Score 415.5; DB 4; Length 210;

Best Local Similarity 66.4%; Pred. No. 5.9e-41;

Matches 89; Conservative 2; Mismatches 10; Indels 33; Gaps 3;

QY 31 VSW-----LFSIVVFGSIWNEGYLNSASEGQFCIYNRPNACSYGVAVGLAFLTCL 83

DB 34 VSWRSRPGCELFSIWVFGSIWNEGYLNSASEGQFCIYNRPNACSYGVAVGLAFLTCL 93

QY 84 LYALDVFYFQISSVKDRKXAVLSDIG-VSGEHPAG----- 119

DB 94 LYALDVFYFQISSVKDRKXAVLSDIG-VSGEHPAG----- 119

QY 120 --TFCTESTEGCGP 131

DB 154 KDNPLNEGTDASPG 167

RESULT 8

AA1067

ID AA1067 standard; protein; 210 AA.

XX AA1067;

AC AA1067;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 5998.

RESULT 9	Db	23	SWLSIVVFGSIWEGYLNASGEQFCIYNRPNACSYGVAVGVLAFITCLLYLALDYY	82
AAM39281				
ID AAM39281 standard; protein; 182 AA.				
XX				
AC AAM39281;	QY	92	FPQISSVKDRKKAVLSDIGVS	112
XX				
DT 22-OCT-2001 (first entry)	Db	83	FPQISSVKDRKKAVLSDIGVS	103
XX				
DE Human polypeptide SEQ ID NO 2426.				
XX				
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;				
KW peripheral nervous system; neuropathy; central nervous system; CNS;				
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;				
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;				
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;				
KW leukaemia.				
XX				
Homo sapiens.				
XX				
WO200153312-A1.				
XX				
26-JUL-2001.				
XX				
26-DEC-2000; 2000WO-US034263.				
XX				
23-DEC-1999; 99US-00471275.				
PR 21-JAN-2000; 2000US-00488725.				
PR 25-APR-2000; 2000US-00552317.				
PR 20-JUN-2000; 2000US-00598042.				
PR 19-JUL-2000; 2000US-00620312.				
PR 03-AUG-2000; 2000US-00653450.				
PR 14-SEP-2000; 2000US-00662191.				
PR 19-OCT-2000; 2000US-00693036.				
PR 29-NOV-2000; 2000US-00727344.				
XX				
(HYSE-) HYSEQ INC.				
XX				
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;				
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;				
PI Zhou P, Goodrich R, Drmanac RT;				
XX				
WPI: 2001-442253/47.				
DR N-PSDB; AAI58437.				
XX				
Novel nucleic acids and polypeptides, useful for treating disorders such				
PT as central nervous system injuries.				
XX				
Example 4; SEQ ID NO 2426; 10078pp; English.				
XX				
The invention relates to human nucleic acids (AAI57798-AAI61369) and the				
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,				
CC immunosuppressant and cytostatic activity. The polynucleotides are useful				
CC in gene therapy. A composition containing a polypeptide or polynucleotide				
CC of the invention may be used to treat diseases of the peripheral nervous				
CC system, such as peripheral nervous injuries, peripheral neuropathy and				
CC localised neuropathies and central nervous system diseases, such as				
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic				
CC utilisation of the activities such as: Immune system suppression,				
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic				
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,				
CC assays for receptor activity, arthritis and inflammation, leukaemias and				
CC C.N.S disorders. Note: The sequence data for this patent did not form				
CC part of the printed specification				
XX				
Sequence 182 AA;				
XX				
Query Match 58.7%; Score 413; DB 4; Length 182;				
Best Local Similarity 98.8%; Pred. No. 9.7e-41;				
Matches 80; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
XX				
32 SWLSIVVFGSIWEGYLNASGEQFCIYNRPNACSYGVAVGVLAFITCLLYLALDYY				
91				

CC the printed specification, but was obtained in electronic format directly  
from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 234 AA;  
Query Match 57.4%; Score 403.5; DB 8; Length 234;  
Best Local Similarity 91.0%; Pred. No. 1.8e-39;  
Matches 81; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

QY 31 VSW-----LFSIVVFGSIVNEGVLNSASGEQFCIYNRNPNACSYGVAVGLAFLTCL 83  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 25 VSMRSPGCELSFIVVFGSIVNEGVLNSASGESEFCIYNRNPNACSYGVAVGLAFLTCL 84  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 84 LYLALDVPFPQISSVKDRKKAVALSDIGVS 112  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 85 LYLALDVPFPQISSVKDRKKAVALSDIGVS 113  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12  
ABG26417  
ID ABG26417 standard; protein; 217 AA.  
XX AC ABG26417;  
XX DT 18-FEB-2002 (first entry)  
XX DE Novel human diagnostic protein #26408.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KM food supplement; medical imaging; diagnostic; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US008631.  
XX PR 31-MAR-2000; 2000US-00540217.  
XX PR 23-AUG-2000; 2000US-00649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI; 2001-639362/73.  
XX DR N-PSDB; AAS90604.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX PS Claim 20; SEQ ID NO 56776; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have application in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic





















Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Garritsen ME;  
 PI Goddard A, Gudowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Kijavich IJ, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA, Shelton DL;

PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI; 2003-328499/31.  
 DR N-PSDB; ACA71759.  
 XX  
 PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as  
 PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying  
 PT modulators of receptor-ligand interactions.  
 XX  
 XX Claim 12; SEQ ID NO 162; 55pp; English.  
 PS  
 XX The invention relates to an isolated secreted and transmembrane  
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful  
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for  
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an  
 CC antibody against it is useful for modulating a biological activity of a  
 CC cell. The PRO polypeptide is useful in industrial applications including  
 CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO  
 CC polypeptide is also useful as a thrombolytic agent, interferon,  
 CC interleukin, erythropoietin, colony stimulating factor and other  
 CC cytokines. The PRO polypeptide is useful for treating disease such as  
 CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,  
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,  
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,  
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and  
 CC myocardial ischaemia; kidney disease e.g. renal failure and  
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial  
 CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory  
 CC bowel disease; reproductive disorders e.g. premature labour and  
 CC pre-eclampsia; carcinogenesis. The present sequence represents the amino  
 CC acid sequence of a PRO polypeptide of the invention. Note: The sequence  
 CC data for this patent did not form part of the printed specification but  
 CC was obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20020177553  
 XX  
 SQ Sequence 224 AA;  
 Query Match 42.1%; Score 296; DB 6; Length 224;  
 Best Local Similarity 48.6%; Pred. No. 1.3e-26;  
 Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;  
 QY 1 MEGAYGAGKAGGAFDPTLVROPHTTLRVVSLFISIVVFGSVNKGILNSAGEQFCI 60  
 DB 1 MEGAYGAGKAGGAFDPTLVROPHTTLRVVSLFISIVVFGSVNKGILNSAGEQFCI 60  
 QY 61 YNRNPACSYGAVGVLAFLTCLLYLALDLYFPQISVKDKKXVLSDI 109  
 DB 61 FNRNEDACRYGSAIGVLAFSLASAFFLVDDAYFPQISNATDKKYLVIQDL 109  
 RESULT 27  
 ABU61095  
 ID ABU61095 standard; protein; 224 AA.  
 XX  
 AC ABU61095;  
 XX  
 DT 08-MAY-2003 (first entry)  
 XX  
 DE Human PRO615 polypeptide.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
 KW cardiac insufficiency; nervous system disorder; kidney disorder;  
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;  
 KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;  
 KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;  
 KW cardiant.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002169284-A1.  
 XX  
 XX 14-NOV-2002.  
 PD

XX 16-OCT-2001; 2001US-00978697.  
 PF 81US-00267213.  
 XX 26-MAY-1981;  
 PR 97US-0062250P.  
 PR 17-OCT-1997;  
 PR 03-NOV-1997;  
 PR 13-NOV-1997;  
 PR 21-NOV-1997;  
 PR 10-MAR-1998;  
 PR 11-MAR-1998;  
 PR 11-MAR-1998;  
 PR 11-MAR-1998;  
 PR 12-MAR-1998;  
 PR 13-MAR-1998;  
 PR 17-MAR-1998;  
 PR 20-MAR-1998;  
 PR 20-MAR-1998;  
 PR 20-MAR-1998;  
 PR 20-MAR-1998;  
 PR 25-MAR-1998;  
 PR 26-MAR-1998;  
 PR 27-MAR-1998;  
 PR 27-MAR-1998;  
 PR 27-MAR-1998;  
 PR 27-MAR-1998;  
 PR 30-MAR-1998;  
 PR 26-JUN-1998;  
 PR 07-OCT-1998;  
 PR 07-OCT-1998;  
 PR 02-NOV-1998;  
 PR 06-NOV-1998;  
 PR 20-NOV-1998;  
 PR 07-DEC-1998;  
 PR 22-DEC-1998;  
 PR 05-JAN-1999;  
 PR 05-MAR-1999;  
 PR 08-MAR-1999;  
 PR 10-MAR-1999;  
 PR 12-MAR-1999;  
 PR 12-APR-1999;  
 PR 14-MAY-1999;  
 PR 14-MAY-1999;  
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 PR 25-AUG-1999;  
 PR 25-AUG-1999;  
 PR 25-AUG-1999;  
 PR 30-NOV-1999;  
 PR 02-DEC-1999;  
 PR 02-DEC-1999;  
 PR 16-DEC-1999;  
 PR 30-DEC-1999;  
 PR 30-DEC-1999;  
 PR 05-JAN-2000;  
 PR 06-JAN-2000;  
 PR 06-JAN-2000;  
 PR 11-FEB-2000;  
 PR 18-FEB-2000;  
 PR 24-FEB-2000;  
 PR 10-MAR-2000;  
 PR 21-MAR-2000;  
 PR 30-MAR-2000;  
 PR 17-MAY-2000;  
 PR 22-MAY-2000;  
 PR 30-MAY-2000;  
 PR 02-JUN-2000;  
 PR 28-JUL-2000;  
 PR 08-AUG-2000;  
 PR 27-NOV-2000;  
 PR 01-DEC-2000;  
 81US-00267213.  
 97US-0062250P.  
 97US-0064249P.  
 97US-0065311P.  
 97US-0066364P.  
 98US-0077450P.  
 98US-0077632P.  
 98US-0077641P.  
 98US-0077649P.  
 98US-0077791P.  
 98US-0078004P.  
 98US-00040220.  
 98US-0078886P.  
 98US-0078910P.  
 98US-0078936P.  
 98US-0078939P.  
 98US-0079294P.  
 98US-0079656P.  
 98US-0079663P.  
 98US-0079664P.  
 98US-0079689P.  
 98US-0079728P.  
 98US-0079786P.  
 98US-0079920P.  
 98US-0079923P.  
 98US-00105413.  
 98US-00168978.  
 98WO-US021141.  
 98US-00184216.  
 98US-00187368.  
 98WO-US024855.  
 98US-00202054.  
 98US-00218517.  
 98WO-US000106.  
 98US-00254465.  
 98WO-US005028.  
 99US-00285686.  
 99WO-US005190.  
 99US-00284291.  
 99US-00311832.  
 99WO-US010733.  
 99WO-US012252.  
 99US-00380137.  
 99US-00380138.  
 99US-00380142.  
 99WO-US028313.  
 99WO-US028551.  
 99WO-US028565.  
 99WO-US030095.  
 99WO-US031243.  
 99WO-US031274.  
 2000WO-US000219.  
 2000WO-US000277.  
 2000WO-US000376.  
 2000WO-US003565.  
 2000WO-US004341.  
 2000WO-US005004.  
 2000WO-US005841.  
 2000WO-US006319.  
 2000WO-US007532.  
 2000WO-US008439.  
 2000WO-US013705.  
 2000WO-US014042.  
 2000WO-US014941.  
 2000WO-US015264.  
 2000WO-US020710.  
 2000WO-US023328.  
 2000US-00709238.  
 2000US-00723749.  
 2000WO-US032678.



Thu Aug 11 17:05:13 2005

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PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US015692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2003-288163/28.
XX N-PSDB; ABX92399.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating cancer, kidney diseases, bone,
XX cartilage disorders and immune deficiencies.
XX
XX Claim 12; Fig 61; 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for linking
XX bioactive molecules to cells expressing PRO polypeptides, for modulating
XX biological activities of cells expressing PRO polypeptides, and for
XX identifying agonists or antagonists. The bioactive molecule maybe a
XX toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
XX The PRO polypeptides are useful for treating immune disorders, diabetes
XX or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
XX disorders, kidney disorders, bone and cartilage disorders or arthritis,
XX tumours, and wound healing. The polynucleotide sequences encoding PRO
XX polypeptides are useful as hybridisation probes, in chromosome and gene
XX mapping, in the generation of antisense RNA and DNA, in the preparation
XX of PRO polypeptides, for generating transgenic animals or knockout
XX animals, for the genetic analysis of individuals with genetic disorders,
XX and in gene therapy. ABU61071-ABU61164 represent the human PRO
XX polypeptides of the invention. Note: The sequence data for this patent
XX was obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/peipsDIDEntry.html
XX
XX Sequence 224 AA;
XX
XX Query Match 42.1%; Score 296; DB 6; Length 224;
XX Best Local Similarity 48.6%; Pred. No. 1.3e-26;
XX Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
XX
XX 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVFGSIVNEGYSASGEQFCI 60
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX
XX 1 MESGAYGAAGAGGSDLRRLFTQPVVARAVCLVFLVIFSCYEGGYNAHESKQYCV 60
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX
XX 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVFFPOISSVKDRKAVLSDI 109
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX
XX 61 FNRNEDACRYGSAIGVLAFLASAFVLYVDYFPOISNATDRKRLVIGDL 109
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX
XX RESULT 28

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ABU80364
ID ABU80364 standard; protein; 224 AA.
XX
XX AC ABU80364;
XX
XX DT 24-JUN-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO615.
XX
XX KW Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;
XX ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;
XX inflammatory disease; necrosis; atherosclerosis; infertility;
XX premature aging; psoriasis; inflammation; inflammatory disease; renal disease;
XX arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;
XX multiple sclerosis; gene therapy.
XX
XX OS Homo sapiens.
XX
XX FN US2003004102-A1.
XX
XX PD 02-JAN-2003.
XX
XX 15-OCT-2001; 2001US-00978189.
XX
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078862P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 25-MAR-1998; 98US-0078939P.
XX 26-MAR-1998; 98US-0079294P.
XX 27-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 30-MAR-1998; 98US-0079920P.
XX 26-JUN-1998; 98US-0079923P.
XX 07-OCT-1998; 98US-00105413.
XX 07-OCT-1998; 98US-00168978.
XX 02-NOV-1998; 98WO-US021141.
XX 02-NOV-1998; 98US-00184216.
XX 08-NOV-1998; 98US-00187368.
XX 20-NOV-1998; 98WO-US024855.
XX 07-DEC-1998; 98US-00202054.
XX 22-DEC-1998; 98US-00218517.
XX 05-JAN-1999; 99WO-US000106.
XX 05-MAR-1999; 99US-00254465.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-00265686.
XX 10-MAR-1999; 99WO-US005190.
XX 12-MAR-1999; 99US-00267213.
XX 12-APR-1999; 99US-00284291.
XX 14-MAY-1999; 99US-00311832.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 25-AUG-1999; 99US-00380137.
XX 25-AUG-1999; 99US-00380138.
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 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrera N, Filvaroff EP, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tumas D, Williams PM, Wood WL;  
 XX WPI; 2003-503575/47.  
 DR N-PSDB; ACD29741.  
 XX Novel secreted and transmembrane polypeptide for modulating biological  
 DR activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers.  
 PT Claim 12; Fig 61; 459pp; English.  
 CC The invention describes an isolated, secreted and transmembrane  
 CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting  
 CC linking a bioactive molecule to a cell expressing the above polypeptides.  
 CC The bioactive molecule is a toxin, radiolabel or an antibody and causes  
 CC cell death. (I) is useful as therapeutic agent, in medical and industrial  
 CC applications e.g. for treating neuropathy, especially peripheral  
 CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,  
 CC Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinemia,  
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XX
PA (GETH ) GENENTECH INC.
XX
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PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

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XX
KW Human; secreted and transmembrane protein; PRO; viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW retinitis pigmentosa; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease.
XX
OS Homo sapiens.
XX
PN US2003049633-A1.
XX
PD 13-MAR-2003.
XX
PP 16-OCT-2001; 2001US-00978585.
XX
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PR 11-MAR-1998; 98US-0077649P.
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PR 22-MAR-2001; 2001WO-US009552.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
PR XX  
PR XX

(GETH ) GENENTECH INC.



PR	10-MAR-1999;	99US-00265686.	QY	1	MEGGAYGAGKAGGAFDPYTLVRQPHHTILRVSWLFSIVVFGSIVNEGYLSASEGEQFCI	60
PR	10-MAR-1999;	99WO-US005190.	Db	1	MESGAYGAKAGGSGDLRRFLTQPVVARAVCLVFLVFSIYGEYSNAHESKQMYCV	60
PR	12-MAR-1999;	99US-00267213.				
PR	12-MAR-1999;	99US-0126773P.				
PR	29-MAR-1999;	99US-0126773P.				
PR	12-APR-1999;	99US-00284291.	QY	61	YNRNPACSYGAVGVLAFLTLCLYLALDVPFPQISSVKDRKKAVLSDI	109
PR	26-APR-1999;	99US-0130232P.	Db	61	FNREDACRYGSAIGVLAFLASAPFLVVDAYFPQISNATDRKYLVIIGDL	109
PR	26-APR-1999;	99US-0131022P.				
PR	28-APR-1999;	99US-0131445P.				
PR	14-MAY-1999;	99US-00311832.				
PR	14-MAY-1999;	99US-0134287P.				
PR	14-MAY-1999;	99WO-US010733.	RESULT 37			
PR	02-JUN-1999;	99WO-US012252.	ADC63534			
PR	16-JUN-1999;	99US-0139557P.	ID	ADC63534	standard; protein; 224 AA.	
PR	23-JUN-1999;	99US-0141037P.	XX	ADC63534;		
PR	07-JUL-1999;	99US-0142680P.	AC	ADC63534;		
PR	26-JUL-1999;	99US-0145698P.	XX			
PR	28-JUL-1999;	99US-0146222P.	DT	18-DEC-2003	(first entry)	
PR	25-AUG-1999;	99US-00380137.	XX			
PR	25-AUG-1999;	99US-00380138.	DE		Human secreted/transmembrane protein, PRO615.	
PR	25-AUG-1999;	99US-00380142.	XX			
PR	29-OCT-1999;	99WO-0162506P.	KW		Human; secreted protein; transmembrane protein; PRO; cytostatic;	
PR	30-NOV-1999;	99WO-US028313.	KW		ophthalmological; antiarthritic; osteopathic; antineumatic; vulnery;	
PR	02-DEC-1999;	99WO-US028551.	KW		auditory; tumour growth; retinal disorder; sports-related joint problem;	
PR	02-DEC-1999;	99WO-US028565.	KW		articular cartilage defects; osteoarthritis; rheumatoid arthritis;	
PR	16-DEC-1999;	99WO-US030095.	KW		wound healing; hearing loss.	
PR	30-DEC-1999;	99WO-US031243.	XX			
PR	30-DEC-1999;	99WO-US031274.	OS		Homo sapiens.	
PR	05-JAN-2000;	2000WO-US000219.	XX			
PR	06-JAN-2000;	2000WO-US000277.	PN		US2003054405-A1.	
PR	06-JAN-2000;	2000WO-US000376.	XX			
PR	11-FEB-2000;	2000WO-US0003565.	PD		20-MAR-2003.	
PR	18-FEB-2000;	2000WO-US004341.	XX			
PR	24-FEB-2000;	2000WO-US005004.	PF		24-OCT-2001; 2001US-00999833.	
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PR	10-MAR-2000;	2000WO-US006319.	PR	17-OCT-1997;	97US-0062250P.	
PR	30-MAR-2000;	2000WO-US008439.	PR	03-NOV-1997;	97US-0064249P.	
PR	17-MAY-2000;	2000WO-US013705.	PR	13-NOV-1997;	97US-0065311P.	
PR	22-MAY-2000;	2000WO-US014042.	PR	21-NOV-1997;	97US-0066364P.	
PR	30-MAY-2000;	2000WO-US014941.	PR	10-MAR-1998;	98US-0077450P.	
PR	28-JUL-2000;	2000WO-US015264.	PR	11-MAR-1998;	98US-0077632P.	
PR	24-AUG-2000;	2000WO-US020710.	PR	11-MAR-1998;	98US-0077641P.	
PR	08-NOV-2000;	2000WO-US023328.	PR	12-MAR-1998;	98US-0077791P.	
PR	27-NOV-2000;	2000US-00723749.	PR	13-MAR-1998;	98US-0078004P.	
PR	01-DEC-2000;	2000WO-US032678.	PR	17-MAR-1998;	98US-00040220.	
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PR	22-MAR-2001;	2001US-00816744.	PR	20-MAR-1998;	98US-0078936P.	
PR	22-MAR-2001;	2001WO-US0015920.	PR	25-MAR-1998;	98US-0079294P.	
PR	10-MAY-2001;	2001WO-US009552.	PR	26-MAR-1998;	98US-0079656P.	
PR	10-MAY-2001;	2001US-00854208.	PR	27-MAR-1998;	98US-0079663P.	
PR	25-MAY-2001;	2001US-00854280.	PR	27-MAR-1998;	98US-0079689P.	
PR	01-JUN-2001;	2001US-00872035.	PR	27-MAR-1998;	98US-0079728P.	
PR	05-JUN-2001;	2001WO-US017800.	PR	30-MAR-1998;	98US-0079920P.	
PR	14-JUN-2001;	2001US-00874503.	PR	30-MAR-1998;	98US-0079923P.	
PR	19-JUN-2001;	2001US-00882636.	PR	31-MAR-1998;	98US-0080105P.	
PR	20-JUN-2001;	2001US-00886342.	PR	31-MAR-1998;	98US-0080107P.	
PR	29-JUN-2001;	2001WO-US019692.	PR	31-MAR-1998;	98US-0080165P.	
PR	09-JUL-2001;	2001WO-US021066.	PR	01-APR-1998;	98US-0080194P.	
PR	30-JUL-2001;	2001WO-US021735.	PR	01-APR-1998;	98US-0080327P.	
PR			PR	01-APR-1998;	98US-0080328P.	
PR			PR	01-APR-1998;	98US-0080333P.	
PR			PR	01-APR-1998;	98US-0080334P.	
PR			PR	08-APR-1998;	98US-0081049P.	
PR			PR	08-APR-1998;	98US-0081070P.	
PR			PR	08-APR-1998;	98US-0081071P.	
PR			PR	09-APR-1998;	98US-0081195P.	
PR			PR	09-APR-1998;	98US-0081203P.	
PR			PR	09-APR-1998;	98US-0081229P.	
PR			PR	15-APR-1998;	98US-0081817P.	
PA	(GETH ) GENENTECH INC.					
XX						
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;					

Query Match 42.1%; Score 296; DB 7; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.3e-26;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;





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Db	61	FRNEDACRYGSAIGVLAFLASAFFLWDAYFPQISNATDRKLYVTGDL	109
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ID	ADC66634	standard; protein; 224 AA.	
XX	AC	ADC66634;	
XX	DT	18-DEC-2003 (first entry)	
XX	DE	Human secreted/transmembrane protein, PRO615.	
XX	KW	vulnerary; virucide; neuroprotective; cytostatic; gene therapy;	
KW	KW	tumour cell proliferation inhibitor;	
KW	KW	secreted and transmembrane protein; PRO; viral infection; wound healing;	
KW	KW	tissue growth; muscle generation; muscle regeneration;	
KW	KW	amyotrophic lateral sclerosis; neuropathy; AIDS-associated neuropathy;	
KW	KW	diabetic peripheral neuropathy; chromosome identification; antagonist;	
KW	KW	tissue typing; immunohistochemical staining.	
XX	OS	Homo sapiens.	
XX	XX	US2003060406-A1.	
XX	PD	27-MAR-2003.	
XX	XX	30-JUL-2001; 2001US-00918585.	
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PR	PR	13-NOV-1997; 97US-0065311P.	
PR	PR	21-NOV-1997; 97US-0066364P.	
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PR	PR	11-MAR-1998; 98US-0077632P.	
PR	PR	11-MAR-1998; 98US-0077641P.	
PR	PR	11-MAR-1998; 98US-0077649P.	
PR	PR	12-MAR-1998; 98US-0077791P.	
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PR	PR	20-MAR-1998; 98US-0078886P.	
PR	PR	20-MAR-1998; 98US-0078910P.	
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PR	PR	25-MAR-1998; 98US-0079294P.	
PR	PR	26-MAR-1998; 98US-0079656P.	
PR	PR	27-MAR-1998; 98US-0079663P.	
PR	PR	27-MAR-1998; 98US-0079664P.	
PR	PR	27-MAR-1998; 98US-0079689P.	
PR	PR	27-MAR-1998; 98US-0079728P.	
PR	PR	27-MAR-1998; 98US-0079786P.	
PR	PR	30-MAR-1998; 98US-0079920P.	
PR	PR	30-MAR-1998; 98US-0079923P.	
PR	PR	31-MAR-1998; 98US-0080105P.	
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PR	PR	06-NOV-1998; 98US-00187368.	
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PR	PR	07-DEC-1998; 98US-00202054.	
PR	PR	27-DEC-1998; 98US-00218517.	
PR	PR	05-JAN-1999; 99WO-US000106.	
PR	PR	05-MAR-1999; 99US-00254465.	
PR	PR	08-MAR-1999; 99WO-US005028.	
PR	PR	10-MAR-1999; 99US-00265686.	
PR	PR	10-MAR-1999; 99WO-US0005190.	
PR	PR	12-MAR-1999; 99US-00267213.	
PR	PR	12-APR-1999; 99US-00284291.	
PR	PR	14-MAY-1999; 99US-00311832.	
PR	PR	14-MAY-1999; 99WO-US010733.	
PR	PR	02-JUN-1999; 99WO-US012252.	
PR	PR	25-AUG-1999; 99US-00380137.	
PR	PR	25-AUG-1999; 99US-00380138.	
PR	PR	25-AUG-1999; 99US-00380142.	
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PR	PR	02-DEC-1999; 99WO-US028551.	
PR	PR	02-DEC-1999; 99WO-US028565.	
PR	PR	16-DEC-1999; 99WO-US030095.	
PR	PR	30-DEC-1999; 99WO-US031243.	
PR	PR	30-DEC-1999; 99WO-US031274.	
PR	PR	05-JAN-2000; 2000WO-US000219.	
PR	PR	06-JAN-2000; 2000WO-US000277.	
PR	PR	06-JAN-2000; 2000WO-US000376.	
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PR	PR	18-FEB-2000; 2000WO-US004341.	
PR	PR	24-FEB-2000; 2000WO-US005004.	
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PR	PR	17-MAY-2000; 2000WO-US013705.	
PR	PR	22-MAY-2000; 2000WO-US014042.	
PR	PR	30-MAY-2000; 2000WO-US014941.	
PR	PR	02-JUN-2000; 2000WO-US015264.	
PR	PR	28-JUL-2000; 2000WO-US020710.	
PR	PR	24-AUG-2000; 2000WO-US023328.	
PR	PR	08-NOV-2000; 2000US-00709238.	
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PR	PR	20-DEC-2000; 2000US-00747259.	
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PR	PR	10-MAY-2001; 2001US-00854208.	
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PR	PR	25-MAY-2001; 2001WO-US017092.	
PR	PR	01-JUN-2001; 2001US-00872035.	
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PR	PR	05-JUN-2001; 2001US-00874503.	
PR	PR	14-JUN-2001; 2001US-00882636.	
PR	PR	19-JUN-2001; 2001US-00886342.	
PR	PR	20-JUN-2001; 2001WO-US019692.	
PR	PR	29-JUN-2001; 2001WO-US021066.	
PR	PR	09-JUL-2001; 2001WO-US021735.	
XX		(GETH ) GENENTECH INC.	
XX	PA	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;	
XX	PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;	
PI	PI	Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;	
PI	PI	Klijavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;	
PI	PI	Stewart TA, Tumas D, Williams PM, Wood WI;	
XX	XX	WPI; 2003-596568/56.	
DR	DR	N-PSDB; ADC66633.	
XX	XX	Novel secreted and transmembrane polypeptides and polynucleotides	
PT	PT	encoding them, useful for treating wound healing, tissue growth and	
PT	PT	muscle generation and regeneration, amyotrophic lateral sclerosis or	
PT	PT	neuropathy.	
XX	XX	Claim 12; SEQ ID NO 162; 472pp; English.	
PS	PS	The invention describes an isolated secreted and transmembrane PRO	
XX	CC	polypeptide (I). PRO polypeptide such as PRO213, PRO700, PRO320 or PRO615	
CC	CC	is useful in biotechnological and medical research, as well as in various	
CC	CC	industrial applications. PRO polypeptide such as PRO300, PRO866, PRO703,	
CC	CC	PRO708, PRO320, PRO351, PRO381, PRO615, PRO618, PRO772, PRO853,	
CC	CC	PRO860 or PRO846 is useful for therapeutic purposes. PRO363 is useful	





PR	25-MAR-1998;	98US-0079294P.	PR	28-MAY-1998;	98US-0087106P.
PR	26-MAR-1998;	98US-0079656P.	PR	28-MAY-1998;	98US-0087208P.
PR	27-MAR-1998;	98US-0079663P.	PR	26-JUN-1998;	98US-0090863P.
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PR	27-MAR-1998;	98US-0079688P.	PR	01-JUL-1998;	98US-0091359P.
PR	27-MAR-1998;	98US-0079729P.	PR	30-JUL-1998;	98US-0094651P.
PR	27-MAR-1998;	98US-0079786P.	PR	01-SEP-1998;	98US-0100038P.
PR	30-MAR-1998;	98US-0079920P.	PR	07-OCT-1998;	98WO-US021141.
PR	30-MAR-1998;	98US-0080105P.	PR	20-NOV-1998;	98US-0109304P.
PR	31-MAR-1998;	98US-0080107P.	PR	22-DEC-1998;	98US-0113296P.
PR	31-MAR-1998;	98US-0080165P.	PR	23-DEC-1998;	98US-0113621P.
PR	31-MAR-1998;	98US-0080194P.	PR	05-JAN-1999;	98WO-US000106.
PR	01-APR-1998;	98US-0080327P.	PR	08-MAR-1999;	99WO-US005028.
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PR	01-APR-1998;	98US-0080333P.	PR	12-MAR-1999;	99US-0126773P.
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PR	09-APR-1998;	98US-0081203P.	PR	02-JUN-1999;	99WO-US012252.
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PR	23-APR-1998;	98US-0083336P.	PR	22-MAR-2000;	2000WO-US005841.
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PR	30-APR-1998;	98US-0084366P.	PR	29-JUN-2001;	2001WO-US021066.
PR	05-MAY-1998;	98US-0084369P.	PR	09-JUL-2001;	2001WO-US021735.
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PR	07-MAY-1998;	98US-0084627P.	XX	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;	
PR	07-MAY-1998;	98US-0084639P.	PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;	
PR	07-MAY-1998;	98US-0084640P.	PI	Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;	
PR	07-MAY-1998;	98US-0084643P.	PI	Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;	
PR	07-MAY-1998;	98US-0084644P.	PI	Stewart TA, Tumas D, Williams PM, Wood WI;	
PR	07-MAY-1998;	98US-0084645P.	XX		
PR	13-MAY-1998;	98US-0085339P.	DR	WPI; 2003-695924/66.	
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PR	15-MAY-1998;	98US-0085700P.	XX		
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PR	18-MAY-1998;	98US-0086023P.	XX		
PR	22-MAY-1998;	98US-0086392P.	PT	New isolated secreted and transmembrane PRO polypeptides, useful in the	
PR	22-MAY-1998;	98US-0086414P.	PT	preparation of a medicament for treating a condition responsive to the	
PR	22-MAY-1998;	98US-0086430P.	PT	polypeptide, and as therapeutic agents e.g. vaccines.	
PR	22-MAY-1998;	98US-0086466P.	XX		
PR	22-MAY-1998;	98US-0087099P.	PS	Claim 12; SEQ ID NO 162; 467pp; English.	



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PR 01-JUL-1998; 98US-0091359P.
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PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
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PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
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XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski P, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-657582/62.
DR N-FSDB; ADC67882.
XX
XX Novel secreted and transmembrane polypeptides, designated PRO
PT polypeptides, and polynucleotides encoding them useful for treating
PT kidney diseases, bone, cartilage and retinal disorders.
XX
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PS Claim 12; SEQ ID NO 162; 468pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 94 fully defined sequences as given
CC in the specification (including PRO lacking its associated signal
CC peptide, a PRO extracellular domain with or without its associated signal
CC peptide). Also included are nucleic acids encoding the PRO proteins
CC mentioned above, a vector comprising a PRO nucleic acid, a host cell
CC comprising the vector and producing PRO, a chimeric molecule comprising
CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
Query Match 42.1%; Score 296; DB 7; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.3e-26;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
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Db 1 MESGAYGAKAGGSPDLRRFLTPQVVARAVCLVFLVIFVSCIVGSGYNAHESKQMYCV 60
QY 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVPYPPQISSVDKRVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVDVDFPQISNATDRKYLVTGDL 109
RESULT 42
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ID ADC41203 standard; protein; 224 AA.
XX
AC ADC41203;
XX
DT 18-DEC-2003 (first entry)
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XX
KW Human; secreted protein; transmembrane protein; PRO; cytostatic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnerary;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss.
XX
OS Homo sapiens.
XX
XX US2003072745-A1.
XX
PD 17-APR-2003.
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PF 25-OCT-2001; 2001US-00013929.
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PR	26-JUN-1998;	98US-0091010P.	PR	polypeptide, and as therapeutic agents e.g. vaccines.	
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PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 28-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.

XX (GETH ) GENENTECH INC.
XX
Query Match 42.1%; Score 296; DB 7; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.3e-26;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVWSWLSFVVGSIWVNGYVNSASEGQFCI 60
Db 1 MESGAYGAAGKAGGSPDLRRFLTPQVWARAVCLVFALIVFSCIYGGYNAHESKQMYCV 60
QY 61 YNRNENACSYGVAVGVLAFLTCLLLVLDVYEPQISSVVDKRAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVTGDL 109

RESULT 46
ADD45142
ID ADD45142 standard; protein; 224 AA.
XX
AC ADD45142;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein O43760, SEQ ID NO 10575.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; O43760.
XX
PT New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
```



2





Thu Aug 11 17:05:13 2005

articular cartilage defects; osteoarthritis; rheumatoid arthritis;  
wound healing; hearing loss.  
Homo sapiens.  
US2003203435-A1.  
30-OCT-2003.  
18-OCT-2001; 2001US-00145092.  
30-APR-1998; 98US-0083742P.  
08-MAR-1999; 99WO-US005028.  
23-JUN-1999; 99US-0141037P.  
25-AUG-1999; 99US-00380138.  
18-FEB-2000; 2000WO-US004341.  
30-JUL-2001; 2001US-00918585.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;  
Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
Klavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
Stewart TA, Tumas D, Williams PM, Wood WI;  
WPI; 2003-875642/81.  
N-PSDB; ADE16363.  
New genes, and its encoded secreted and transmembrane polypeptides,  
useful for treating e.g. lung or breast tumors, osteoarthritis,  
rheumatoid arthritis, obesity, diabetes, hyperinsulinemia,  
hypoinsulinemia or wounds.

Claim 12; SEQ ID NO 162; 452pp; English.

The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to an amino acid sequence chosen from 94 fully defined sequences as given in the specification (including PRO lacking its associated signal peptide, a PRO extracellular domain with or without its associated signal peptide). Also included are nucleic acids encoding the PRO proteins mentioned above, a vector comprising a PRO nucleic acid, a host cell comprising the vector and producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. PRO337 polypeptide is useful for detecting a PRO4993 polypeptide in a sample suspected of containing PRO4993 polypeptide. Similarly, PRO4993 polypeptide is useful for detecting PRO337 polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive molecule is the toxin, radiolabel, or an antibody. The bioactive molecule causes death of the cell. PRO337 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725, PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO725, PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337 polypeptide is useful for modulating at least one biological activity of the cell expressing PRO337 polypeptide, where the cell is killed. PRO337 polypeptide or anti-PRO4993 polypeptide is useful for modulating the biological activity of the cell expressing PRO4993 polypeptide, PRO725, PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for modulating the biological activity of the cell expressing PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-PRO739 polypeptide is useful for modulating the biological activity of the cell expressing PRO725, PRO700 or PRO739 polypeptide. The polypeptides are useful for inhibiting tumour growth, retinal disorders, sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in mammals. The present sequence represents a PRO protein.

SQ Sequence 224 AA;

Query Match 42.1%; Score 296; DB 7; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.3e-26;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLVRVSWLFSIVVFGSIVNEGYLNSASEGQFCI 60  
DB 1 MESGAYGAAGAGGSPDLRRFLTPQVVARAVCLVFLVIFVSCYIGGYNAHESKQYCV 60  
QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVPYPPQISSVVKDKKAVLSDI 109  
DB 61 FNRNEDACRYGSAIGVLAFLASAFELVVDAYFPQISNATDRKYLVIIGDL 109

Search completed: August 11, 2005, 08:23:48  
Job time : 167 secs

**This Page Blank (uspto)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 42 Seconds  
(without alignments)  
234.611 Million cell updates/sec

Title: US-10-643-836-297

Perfect score: 703

Sequence: 1 MEGGAYGAGKAGGAFDPTL.....GEPHPAGTPTCTESTGCPGP 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

- Issued Patents AA.\*
- 1: /cgn2\_6/prodata/1/iaa/5A COMB.pgp.\*
  - 2: /cgn2\_6/prodata/1/iaa/5B COMB.pgp.\*
  - 3: /cgn2\_6/prodata/1/iaa/6A COMB.pgp.\*
  - 4: /cgn2\_6/prodata/1/iaa/6B COMB.pgp.\*
  - 5: /cgn2\_6/prodata/1/iaa/6C COMB.pgp.\*
  - 6: /cgn2\_6/prodata/1/iaa/backfileesl.pgp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	82.1	112	4	US-09-513-999C-4379
2	577	82.1	234	4	US-09-949-016-6539
3	519.5	73.9	231	2	US-08-700-637-3
4	296	42.1	224	2	US-08-700-637-2
5	291	41.4	56	4	US-09-621-976-4130
6	100	14.2	63	4	US-09-513-999C-4596
7	82	11.7	907	2	US-09-010-928B-4
8	78	11.1	253	4	US-09-248-796A-15975
9	73	10.4	407	2	US-08-776-585-3
10	73	10.4	407	3	US-08-986-659B-10
11	72	10.2	714	4	US-09-489-039A-11109
12	71.5	10.2	332	4	US-09-659-519-4
13	71.5	10.2	400	1	US-07-783-602C-1
14	71.5	10.2	525	4	US-09-107-532A-5743
15	71	10.1	488	4	US-09-540-236-2307
16	70	10.0	2161	1	US-07-745-206A-2
17	70	10.0	2161	1	US-08-455-543A-49
18	70	10.0	2161	1	US-08-455-543A-51
19	70	10.0	2161	2	US-08-223-305C-49
20	70	10.0	2161	2	US-08-223-305C-51
21	70	10.0	2161	2	US-08-311-363-2
22	70	10.0	2181	4	US-09-949-016-5981
23	70	10.0	2188	4	US-09-949-016-8295
24	69.5	9.9	164	4	US-09-543-681A-5125
25	69.5	9.9	391	5	PCT-US95-15696-2
26	69.5	9.9	400	1	US-07-916-901-6
27	69.5	9.9	400	1	US-08-351-473B-4

28	69.5	9.9	809	5	PCT-US91-01726-3	Sequence 3, Appli
29	69	9.8	18	3	US-09-227-357-510	Sequence 510, App
30	68	9.7	197	4	US-09-252-991A-32320	Sequence 32320, A
31	68	9.7	319	4	US-09-107-532A-6471	Sequence 6471, Ap
32	68	9.7	462	4	US-09-328-352-5497	Sequence 5497, Ap
33	68	9.7	689	4	US-09-949-016-11276	Sequence 11276, A
34	68	9.7	706	4	US-09-134-000C-5534	Sequence 5534, Ap
35	67.5	9.6	436	4	US-09-949-016-11448	Sequence 11448, A
36	67.5	9.6	470	2	US-08-724-394A-10	Sequence 10, Appl
37	67	9.5	507	4	US-09-538-092-354	Sequence 354, App
38	67	9.5	515	4	US-09-170-496D-104	Sequence 104, App
39	67	9.5	515	4	US-09-170-496D-220	Sequence 220, App
40	67	9.5	597	4	US-09-328-352-4703	Sequence 4703, Ap
41	67	9.5	907	4	US-09-198-452A-306	Sequence 306, App
42	67	9.5	928	4	US-09-438-185A-295	Sequence 295, App
43	67	9.5	1252	4	US-10-012-762-20	Sequence 20, Appl
44	67	9.5	1252	4	US-09-704-036B-20	Sequence 20, Appl
45	66.5	9.5	369	4	US-09-519-232-74	Sequence 74, Appl
46	66.5	9.5	378	4	US-09-441-411-8	Sequence 8, Appli
47	66	9.4	237	4	US-09-489-039A-9365	Sequence 9365, Ap
48	66	9.4	244	2	US-09-090-567-2	Sequence 2, Appli
49	66	9.4	317	1	US-08-118-270-10	Sequence 10, Appl
50	66	9.4	317	5	PCT-US93-08528-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-09-513-999C-4379  
; Sequence 4379, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4379  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -41..-1  
; OTHER INFORMATION: score 4.3  
; OTHER INFORMATION: seq RVSWLFSIVVFG/SI  
US-09-513-999C-4379

Query Match 82.1%; Score 577; DB 4; Length 112;  
Best Local Similarity 99.1%; Pred. No. 1.5e-58;  
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGGAYGAGKAGGAFDPTLVRQPHILRVSWLFSIVVFGSIVNKGYNLSASEGSEFCI	60
DB	1	MEGGAYGAGKAGGAFDPTLVRQPHILRVSWLFSIVVFGSIVNKGYNLSASEGSEFCI	60
QY	61	YNRNPACSYGAVGVLAFLTCLLYLALDVFPQISSVKDRKAVLSIDIGVS	112
DB	61	YNRNPACSYGAVGVLAFLTCLLYLALDVFPQISSVKDRKAVLSIDIGVS	112

RESULT 2  
US-09-949-016-6539  
; Sequence 6539, Application US/09949016  
; Patent No. 6812339



## RESULT 5

US-09-621-976-4130  
; Sequence 4130, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4130  
; LENGTH: 56  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -41...-1  
US-09-621-976-4130

Query Match 41.4%; Score 291; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.3e-26;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPTLVLRQPHILRVVSWLFSIVVFGSIVNEGYNLSASEGE 56  
|||||  
DB 1 MEGGAYGAGKAGGAFDPTLVLRQPHILRVVSWLFSIVVFGSIVNEGYNLSASEGE 56  
|||||

## RESULT 6

US-09-513-999C-4596  
; Sequence 4596, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4596  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -39...-1  
; OTHER INFORMATION: score 4.6  
; OTHER INFORMATION: seq AFLSCLAFVLDT/QE  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 19  
; OTHER INFORMATION: Xaa=Cys or Phe or Ile or Leu or Arg or Ser  
US-09-513-999C-4596

Query Match 14.2%; Score 100; DB 4; Length 63;  
Best Local Similarity 42.0%; Pred. No. 0.00043;  
Matches 21; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 59 CIYNRNPNACSYGVAVGLAFELTCLLYLALDVYFPQISSVKORKKAVLSD 108  
|||||  
DB 8 CILNSNSVACSFVAGAGFLAFSLCLAFVLDTQETRIAGTRFKTAFLQD 57  
|||||

## RESULT 7

US-09-010-928B-4  
; Sequence 4, Application US/09010928B  
; Patent No. 5994039  
; GENERAL INFORMATION:  
; APPLICANT: Lewis, Randolph V  
; APPLICANT: Hayashi, Cheryl Y  
; TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA  
; NUMBER OF INVENTION: CODING THEREFOR  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
; STREET: 8110 GATEHOUSE RD. SUITE 500E  
; CITY: FALLS CHURCH  
; STATE: VIRGINIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 22042

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/010,928B  
; FILING DATE: 22-JAN-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy Jr., Gerald M  
; REGISTRATION NUMBER: 28977  
; REFERENCE/DOCKET NUMBER: 1447-109P  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 907 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-010-928B-4

Query Match 11.7%; Score 82; DB 2; Length 907;  
Best Local Similarity 32.9%; Pred. No. 1.7;  
Matches 28; Conservative 14; Mismatches 27; Indels 16; Gaps 5;

QY 3 GGAYGAGKAGGAFDPTLVLRQPHILRVVSWL----FSIVVFGSIVNEGYNLSASEGEQF 58  
|||||  
DB 805 GGAYGSPGAYYPSS--RVPDMVNGINSAMQSGFNQMFGNM-----LSQVSSGSGT 857  
|||||  
QY 59 CIYNRNPNACSYGVAVGLAFELTCL 83  
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DB 858 C----NPNVNV-LMDALLAALHCL 877  
|||||

## RESULT 8

US-09-248-796A-15975  
; Sequence 15975, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; OTHER INFORMATION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 15975  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Candida albicans

US-09-248-796A-15975

Query Match 11.1%; Score 78; DB 4; Length 253;  
Best Local Similarity 24.5%; Pred. No. 0.9;  
Matches 24; Conservative 17; Mismatches 35; Indels 22; Gaps 2;  
QY 14 AFDPYTLVLRQPHILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI-YNRNPNAC 69  
Db 126 AYDEYTKPLGRLPEKSKRLILLDLFIFFSANLSLAFNTWDDVWCKANKTGLAD 185  
QY 70 YGVAVGLAFLTCLLYLALDVYFPQISSVKDRKKAVL 107  
Db 186 IGVA-----EFTIGSICRRQRLSS 205

RESULT 9  
US-08-776-585-3  
; Sequence 3, Application US/08776585  
; Patent No. 5932426  
; GENERAL INFORMATION:  
; APPLICANT: BARALLE, Francesco E.  
; APPLICANT: SCODELLER, Eduardo  
; APPLICANT: TIMINETZKY, Sergio  
; TITLE OF INVENTION: MOLECULAR PRESENTING SYSTEM  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/776,585  
; FILING DATE: 31-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/03114  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ISACSON, John P.  
; REGISTRATION NUMBER: 33,715  
; REFERENCE/DOCKET NUMBER: 69582/106  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 407 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-776-585-3

Query Match 10.4%; Score 73; DB 2; Length 407;  
Best Local Similarity 28.9%; Pred. No. 6.3;  
Matches 35; Conservative 15; Mismatches 57; Indels 14; Gaps 5;  
QY 12 GGAFDPYTLVRQPHILRVVSW--LFSIVVFGSIVNVEGYLNSASEGEQFCI-YNRNPNAC 68  
Db 270 GSTGQPTMTDSGAETSIVVVGWGNMDTIVIRVS-APEGAVNSAILKAWSCIEYRPNPNAM 328  
QY 69 SYGVA-----VGVLAFLTCLLYLALDVYFPQISSVKDRKKAVL--SDIGVSGEPHPA 118  
Db 329 LYQFGHDSPLDEVALQEQYRTVARSPLFVAVIAAQNASMMWVKSIKSSLAASNPGP 388  
QY 119 G 119

Db 389 G 389

RESULT 10  
US-08-986-659B-10  
; Sequence 10, Application US/08986659B  
; Patent No. 6171591  
; GENERAL INFORMATION:  
; APPLICANT: Hall, Stephen G.  
; TITLE OF INVENTION: RECOMBINANT NODAVIRUS RELATED  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. 6171591th Wacker Drive, 36th Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,659B  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Talivaldis Cepuritis  
; REGISTRATION NUMBER: 20,818  
; REFERENCE/DOCKET NUMBER: 549.0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-580-1180  
; TELEFAX: 312-580-1189  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 407 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: N/A  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-986-659B-10

Query Match 10.4%; Score 73; DB 3; Length 407;  
Best Local Similarity 28.9%; Pred. No. 6.3;  
Matches 35; Conservative 15; Mismatches 57; Indels 14; Gaps 5;  
QY 12 GGAFDPYTLVRQPHILRVVSW--LFSIVVFGSIVNVEGYLNSASEGEQFCI-YNRNPNAC 68  
Db 270 GSTGQPTMTDSGAETSIVVVGWGNMDTIVIRVS-APEGAVNSAILKAWSCIEYRPNPNAM 328  
QY 69 SYGVA-----VGVLAFLTCLLYLALDVYFPQISSVKDRKKAVL--SDIGVSGEPHPA 118  
Db 329 LYQFGHDSPLDEVALQEQYRTVARSPLFVAVIAAQNASMMWVKSIKSSLAASNPGP 388  
QY 119 G 119  
Db 389 G 389

RESULT 11  
US-09-489-039A-11109  
; Sequence 11109, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

```

; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11109
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-11109

Query Match      10.2%; Score 72; DB 4; Length 714;
Best Local Similarity 25.2%; Pred. No. 17;
Matches 31; Conservative 19; Mismatches 49; Indels 24; Gaps 5;

QY 9 GKAGAFDPTLVQP-----H-TILRVSWLFSIVVFGSIVNVEGYLNSAGEQ--- 57
DB 6 GSHAGPAPAAARERACRYRHLCVSRPVSIFIVHOF-----NRAQEEVQVVF 56
QY 58 ---FCIYNRPNACSYGAVGLAFITCLLYLALDVVFPQISSVKDKKAVLSDIGV-SG 113
DB 57 DRFFHLHLFPVQAAGVADARLTMLNLVALSVIAAFHTFAGERREARIAQRMTFEAG 116
QY 114 EPH 116
DB 117 EQH 119

RESULT 12
US-09-659-519-4
; Sequence 4, Application US/09659519
; Patent No. 6783973
; GENERAL INFORMATION:
; APPLICANT: Grandy, David K
; APPLICANT: Bunzow, James R
; TITLE OF INVENTION: Mammalian Catecholamine Receptor Genes and Uses
; FILE REFERENCE: Catecholamine receptor genes
; CURRENT APPLICATION NUMBER: US/09/659,519
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-659-519-4

Query Match      10.2%; Score 71.5; DB 4; Length 332;
Best Local Similarity 25.7%; Pred. No. 7.1;
Matches 26; Conservative 19; Mismatches 37; Indels 19; Gaps 6;

QY 27 ILRVSW-LFSIVVFGSIVNVEGYLNSASE---GEQFCIYNRPNAC--SYGVAVGVLAPL 80
DB 141 WMLISWLPVAFPAFGMIFLELNLEGVEEQYHNVQVCL-----RGCFLFESKVSGLVAFM 195
QY 81 T-----CLLYLALDVVFPQISSVKDKKAVLSDIGVSGE 114
DB 196 TSFYIPGVMFLFVYIYFIYFAKQARSINRANL-QVGLGE 235

RESULT 13
US-07-783-602C-1
; Sequence 1, Application US/07783602C
; Patent No. 5418160
; GENERAL INFORMATION:
; APPLICANT: J. Craig Venter et al
; TITLE OF INVENTION: A FAT CELL SPECIFIC a-ADRENERGIC
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza

```

```

; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/783,602C
; FILING DATE: 19911101
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: J.G. Mullins
; REGISTRATION NUMBER: 33073
; TELEPHONE/DOCKET NUMBER: 717-098
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
; US-07-783-602C-1

Query Match      10.2%; Score 71.5; DB 1; Length 400;
Best Local Similarity 26.0%; Pred. No. 9.1;
Matches 39; Conservative 19; Mismatches 51; Indels 41; Gaps 9;

QY 14 AFDPTLVQPHTILR-----VVSWLFSIVV-FGSIYNEGYNLSAGEQF 58
DB 129 AVDRILAVTNP---LRYGTLVTKRRARAVALVIVSATVSPAPINSMWRVGCADAEQ 185
QY 59 CIYNRPNACS-----YGVAVGVLAFLTCLLYLALDVVFPQISSVKDKKAVLSDIG-- 110
DB 186 C--HSNPRCCSPASNMPYALLSSVSFYLPPLVM-LFVYARVVFVAKQRFRFVRELGRF 242
QY 111'-----VSGRPHRA--CTPCTESTEGCP 130
DB 243 PPEESPRSPSPSPATVGTGTP--TASDGV 270

RESULT 14
US-09-107-532A-5743
; Sequence 5743, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571

```

```
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5743:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...525
; SEQUENCE DESCRIPTION: SEQ ID NO: 5743:
US-09-107-532A-5743

Query Match 10.2%; Score 71.5; DB 4; Length 525;
Best Local Similarity 23.1%; Pred. No. 13;
Matches 33; Conservative 19; Mismatches 34; Indels 57; Gaps 7;

QY 10 KAGGAFDPYTLRQPHILRVSWLFSIVVFGSIVNEG---YNSASEGEQFCIVNR--- 63
Db 235 KAGGAFQSTLV-----CKLIP-LFVIVIFGLFRQGVDFQLFPIQAGENLSFFSALGA 287
QY 64 -----NPNACSYGVAVGVLAFLTCLLYLALDVYFPPI 95
Db 288 GLLATMFAYDGMWIVHGNISGELKKPKADLPKATISLGI-IGIM-----IVLLVNAVFLRT 341
QY 96 SSVKDRKKAVLSDIGVSGEPHPA 118
Db 342 ASID-----GVAGNSNA 354

RESULT 15
US-09-540-236-2307
; Sequence 2307, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2307
; LENGTH: 488
; TYPE: PRT
; ORGANISM: M.catarrhalis
; US-09-540-236-2307

Query Match 10.1%; Score 71; DB 4; Length 488;
Best Local Similarity 24.6%; Pred. No. 14;
Matches 28; Conservative 12; Mismatches 28; Indels 46; Gaps 7;

QY 31 VSWLFSI-VVFGSIVNEGYNLSASEGEQFCIVNRNPNACSYGVAVGVLAFLTCLLYALD 89
Db 208 MTWIFFILIVFTQTNAGYMR-----EIMCVY-----ICPYG----- 239
QY 90 VYFQISSVK-DRKXAVLSDIGVSGEPH-----PAG-----TPCTESTEGCP 130
Db 240 -----RFQSVMFQDKTLTVSYDYERGERPRGARKKDTTPAGYGDVCDCTMCVQVCP 289

RESULT 16
US-07-745-206A-2
```

```
; Sequence 2, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745,206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-745-206A-2

Query Match 10.0%; Score 70; DB 1; Length 2161;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYCAGKAGGAFDPYTL-----VRQPHILRVSWLFSIVVFGSIVNEGYNLSASEGRQ 57
Db 222 EGNHSSGKSGG-FDVKALRAFVLRP---LRKNSGVSLQV-----VLNS----- 263
QY 58 FCIVNRNPNACSYGVAVGVLAFLTCLLYALDVYFP-----QISSVKDRKKAVLS 108
Db 264 -----IIKAWVPLHLIALVLFVIIYAIIGLELFIGKWHKTCFFAD 305
QY 109 IGVSGEPHPAGTFC-----TESTEGCPG 132
Db 306 SDIVAEEDPA--PCAFSGNGROCTANGTECRSGWVGP 340

RESULT 17
US-08-455-543A-49
; Sequence 49, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
```



```

; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-49

Query Match 10.0%; Score 70; DB 1; Length 2161;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

Qy 2 EGGAYGAGKAGAFDPYTL-----VRPHHTILRVVSWLFSIVVFGSIYNEGYLNSASGEQ 57
Db 222 EGGHSSKSGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263
Qy 58 FCINRNPACSGYGVAVGLAFLTCLLYLALDVYFP-----QISSVKDRKAVLSD 108
Db 264 -----IIRKAVPLLIALLVLIIVAIIGLELFIQGMHKTCTFFAD 305
Qy 109 IGVSGEHPACTPC-----TESTEGCPCP 132
Db 306 SDIVAEEDPA--PCAFSGNGRQCTANGTECRSGWGP 340

; Sequence 51, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-455-543A-51

Query Match 10.0%; Score 70; DB 1; Length 2161;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

Qy 2 EGGAYGAGKAGAFDPYTL-----VRPHHTILRVVSWLFSIVVFGSIYNEGYLNSASGEQ 57
US-08-455-543A-51
```

```
Db      222 EGNHSSGKGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263
QY      58 FCYINRNPACSYGVAVGVLAFTCLLYLALDYVFP-----QISSVKDRKKAVLSD 108
Db      264 -----IKAMVPLHLIALLVFVIIIIYAIIGLELFTGKVKHKTCTFFAD 305
QY      109 IGVSGEPHPAGTPC-----TESTGCPGP 132
Db      306 SDIVAEEDPA--PCAFSGNGROQTANGTECRSGWVGP 340

RESULT 19
US-08-223-305C-49
; Sequence 49, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; FILING DATE: April 10, 1992
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0899
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-49

Query Match      10.0%; Score 70; DB 2; Length 2161;
Best Local Similarity 25.5%; Pred No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY      2 EGGAYGAGKAGGAFDPYTL----VRQPHITLKVWSWLFPSIVVFGSIVNMGYNLSASEGQ 57
Db      222 EGNHSSGKGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263
QY      58 FCYINRNPACSYGVAVGVLAFTCLLYLALDYVFP-----QISSVKDRKKAVLSD 108
Db      264 -----IKAMVPLHLIALLVFVIIIIYAIIGLELFTGKVKHKTCTFFAD 305
QY      109 IGVSGEPHPAGTPC-----TESTGCPGP 132
Db      306 SDIVAEEDPA--PCAFSGNGROQTANGTECRSGWVGP 340

RESULT 20
US-08-223-305C-51
; Sequence 51, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-51

Query Match 10.0%; Score 70; DB 2; Length 2161;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYGAGKAGGAFDPYTL-----VRPHTILRVVSMFLFSIVVFGSIVNEGYNLSASEGEQ 57
Db 222 EGGHSSGKSGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263

QY 58 FCYINRPNACSYGVAVGLAFLTCLLYLALDVYFP-----QISSVKDKRKKAVLSD 108
Db 264 -----IHKMVPPLLHIALLVLFVIIYAIIGLELFGIKHKTCTFFAD 305

QY 109 IGVSGEPHPAGTPC-----TESTEGCPGP 132
Db 306 SDIVAEEDPA--PCAFSGNGRQCTANGTECRSGWVGP 340

RESULT 21
US-08-311-363-2
; Sequence 2, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-311-363-2

Query Match 10.0%; Score 70; DB 2; Length 2161;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYGAGKAGGAFDPYTL-----VRPHTILRVVSMFLFSIVVFGSIVNEGYNLSASEGEQ 57
Db 222 EGGHSSGKSGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263

QY 58 FCYINRPNACSYGVAVGLAFLTCLLYLALDVYFP-----QISSVKDKRKKAVLSD 108
Db 264 -----IHKMVPPLLHIALLVLFVIIYAIIGLELFGIKHKTCTFFAD 305

QY 109 IGVSGEPHPAGTPC-----TESTEGCPGP 132
Db 306 SDIVAEEDPA--PCAFSGNGRQCTANGTECRSGWVGP 340

RESULT 22
US-09-949-016-5981
; Sequence 5981, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5981
; LENGTH: 2181
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-5981

Query Match 10.0%; Score 70; DB 4; Length 2181;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYGAGKAGGAFDPYTL-----VRPHTILRVVSMFLFSIVVFGSIVNEGYNLSASEGEQ 57
Db 222 EGGHSSGKSGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263

QY 58 FCYINRPNACSYGVAVGLAFLTCLLYLALDVYFP-----QISSVKDKRKKAVLSD 108
Db 264 -----IHKMVPPLLHIALLVLFVIIYAIIGLELFGIKHKTCTFFAD 305

QY 109 IGVSGEPHPAGTPC-----TESTEGCPGP 132
Db 306 SDIVAEEDPA--PCAFSGNGRQCTANGTECRSGWVGP 340

RESULT 23
US-09-949-016-8295
; Sequence 8295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```



;/ ZIP: 48099  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent In Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/07/916,901  
;/ FILING DATE: 19920720  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Kohn, Kenneth I.  
;/ REGISTRATION NUMBER: 30,955  
;/ REFERENCE/DOCKET NUMBER: P-324 (WSU)  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (313) 689-3554  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 400 amino acids  
;/ TYPE: AMINO ACID  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ US-07-916-901-6

Query Match 9.9%; Score 69.5; DB 1; Length 400;  
Best Local Similarity 25.3%; Pred. No. 15;  
Matches 38; Conservative 20; Mismatches 51; Indels 41; Gaps 9;

QY 14 AFDPYTLVRQPHILR-----VSWLFSIVV-FGSIYNEGYLSASGEQF 58  
DB 129 AVDRYLAVTNP---LRYGTLVTKRRARAAVLVWIVSATVSFAPIMSQWVRVGADAEAOE 185

QY 59 CIYNRNPAC-----YGVAVGVLAFLTCLLYLALDVTFFPQISSVKDRKKAVLSDIG-- 110  
DB 186 C--HSNPRCCSFASNNPYALLSSVSFYLLPLVM-LFVYARVFWAKRQRLRLRELGRF 242

QY 111 -----VSGEPHFA--GTPCTESTEGCP 130  
DB 243 PPESPRSPRSFSPATVGTGTP--TASDGV 270

RESULT 27  
US-08-351-473B-4  
; Sequence 4, Application US/08351473B  
; Patent No. 5656440  
; GENERAL INFORMATION:  
; APPLICANT: LENZEN, GERLINDA  
; APPLICANT: KAPOOR, ARCHANA  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE  
; TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/351,473B  
; FILING DATE: 21-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 93 04670  
; FILING DATE: 21-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR94/00447  
; FILING DATE: 21-APR-1994

;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: OBLON, NORMAN F.  
;/ REGISTRATION NUMBER: 24,618  
;/ REFERENCE/DOCKET NUMBER: 6639-001-0X PCT  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (703) 413-3000  
;/ TELEFAX: (703) 413-2220  
;/ TELEX: 248855 OPAT UR  
;/ INFORMATION FOR SEQ ID NO: 4:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 400 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-351-473B-4

Query Match 9.9%; Score 69.5; DB 1; Length 400;  
Best Local Similarity 25.3%; Pred. No. 15;  
Matches 38; Conservative 20; Mismatches 51; Indels 41; Gaps 9;

QY 14 AFDPYTLVRQPHILR-----VSWLFSIVV-FGSIYNEGYLSASGEQF 58  
DB 129 AVDRYLAVTNP---LRYGTLVTKRRARAAVLVWIVSATVSFAPIMSQWVRVGADAEAOE 185

QY 59 CIYNRNPAC-----YGVAVGVLAFLTCLLYLALDVTFFPQISSVKDRKKAVLSDIG-- 110  
DB 186 C--HSNPRCCSFASNNPYALLSSVSFYLLPLVM-LFVYARVFWAKRQRLRLRELGRF 242

QY 111 -----VSGEPHFA--GTPCTESTEGCP 130  
DB 243 PPESPRSPRSFSPATVGTGTP--TASDGV 270

RESULT 28  
PCT-US91-01726-3  
; Sequence 3, Application PC/TUS9101726  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Malcolm R  
; APPLICANT: Saxena, Inder M  
; APPLICANT: Lin, Fong C  
; TITLE OF INVENTION: Recombinant Cellulose Synthase  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David L. Parker  
; STREET: 600 Congress Avenue Suite 2300  
; CITY: Austin  
; STATE: Texas  
; COUNTRY: United States  
; ZIP: 78701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/01726  
; FILING DATE: 19910314  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 494093  
; FILING DATE: 15-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker Mr. David L  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200  
; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 809 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear



RESULT 31  
US-09-107-532A-6471  
; Sequence 6471, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6471:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 319 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...319  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6471:  
US-09-107-532A-6471

Query Match 9.7%; Score 68; DB 4; Length 319;  
Best Local Similarity 34.2%; Pred. No. 17;  
Matches 27; Conservative 10; Mismatches 26; Indels 16; Gaps 4;

Qy 52 ASEGQFCYNNRPNACSY-----GVAVGLAFLTCLLYALDVPFQISSV-----KDR 101  
Db 38 ASEGRTTMAEN-VPSSCFYNGKSVTNAELRAAGADLILFNLDLPNFIQISGVPLTLKEN 96

Qy 102 -----KKAVLSDIGVSGEP 115

Db 97 PIWIKKALGRAIGNLEP 115

RESULT 32  
US-09-328-352-5497  
; Sequence 5497, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5497  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5497

Query Match 9.7%; Score 68; DB 4; Length 462;  
Best Local Similarity 22.2%; Pred. No. 28;  
Matches 41; Conservative 22; Mismatches 48; Indels 74; Gaps 10;

Qy 3 GGAYGAG-----KAG--GAFDPYTLVRQPHITLRRV-----SW- 33  
Db 162 GGEYGASATYLSMAEKDRRGRFFSFQYVYTLIAGQITALCVLLILQMLITEEQLDHGWGR 221

Qy 34 -----LFSIVP-----GSIVNEGVLNSASGEQ-----FCIYNRPN---ACSYGVAV 74  
Db 222 VPPFFIGALLAIVVFRIRRGLETSQSFKNQAETDOPKSGMFALFKHYPKAEFTVLFITAG 281

Qy 75 GVLAFLTCLLY-----LALDVPF---POISSVKDR---KKAVLSD 108  
Db 282 GTLAFYTYTYTLQKYLNVNTSGFTKPEATQITLALFIFMCLQPLAGALSDRIGRKPIMIA 341

Qy 109 IGVSQ 113

Db 342 FGVTG 346

RESULT 33  
US-09-949-016-11276  
; Sequence 11276, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11276  
; LENGTH: 689  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11276

Query Match 9.7%; Score 68; DB 4; Length 689;  
Best Local Similarity 35.7%; Pred. No. 47;  
Matches 15; Conservative 5; Mismatches 20; Indels 2; Gaps 1;

Qy 93 POISSVKDR---KKAVLSDIGVSGEPHPAGTPCTESTEGCGP 132  
Db 186 PGLQGVKHAGKRGILGDPGHQKPGKGDVGASGEGQIGP 227

RESULT 34  
US-09-134-000C-5534  
; Sequence 5534, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS





6555339-Endogenous, Constitutively Activated Human G Protein

NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 306  
; LENGTH: 907  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-306

Query Match 9.5%; Score 67; DB 4; Length 907;  
Best Local Similarity 24.8%; Pred. No. 88;  
Matches 30; Conservative 15; Mismatches 52; Indels 24; Gaps 6;

QY 14 APDPYTLVRQPHILRVVWMLFSIVVFGSIVN--EGYLSASGEQFCIYNR---NPNAC 68

DB 110 AIDP---PRSPLFYRIVVWMLFSIVVFGSIVN--EGYLSASGEQFCIYNR---NPNAC 166

QY 69 SYGVAV-----GVLAFLTCLLYALDLYVFPQISSVVKDKKAVLSDIGV---SGEPH 116

DB 167 GSGIIASLVHTIGIQLILFTAAVLVT-----FPVIVYVSKSLKSLSDDDHDLFIDTGHPP 222

QY 117 P 117

DB 223 P 223

RESULT 42  
US-09-438-185A-295  
; Sequence 295, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 295  
; LENGTH: 928  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CPn0293  
US-09-438-185A-295

Query Match 9.5%; Score 67; DB 4; Length 928;  
Best Local Similarity 24.8%; Pred. No. 91;  
Matches 30; Conservative 15; Mismatches 52; Indels 24; Gaps 6;

QY 14 APDPYTLVRQPHILRVVWMLFSIVVFGSIVN--EGYLSASGEQFCIYNR---NPNAC 68

DB 110 AIDP---PRSPLFYRIVVWMLFSIVVFGSIVN--EGYLSASGEQFCIYNR---NPNAC 166

QY 69 SYGVAV-----GVLAFLTCLLYALDLYVFPQISSVVKDKKAVLSDIGV---SGEPH 116

DB 167 GSGIIASLVHTIGIQLILFTAAVLVT-----FPVIVYVSKSLKSLSDDDHDLFIDTGHPP 222

QY 117 P 117

DB 223 P 223

RESULT 43  
US-10-012-762-20  
; Sequence 20, Application US/10012762  
; Patent No. 6635438  
; GENERAL INFORMATION:  
; APPLICANT: KAWASAKI, GLENN  
; APPLICANT: WEBB, HEATHER K.  
; APPLICANT: OWENS, JEFFREY  
; APPLICANT: LIEDTKE, RAYMOND  
; APPLICANT: FOREST, DOREEN  
; APPLICANT: LEGAZ, MARK  
; APPLICANT: LAWSON, SOBOMABO  
; TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE  
; FILE REFERENCE: 30865  
; CURRENT APPLICATION NUMBER: US/10/012,762  
; CURRENT FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: 60/163,126  
; PRIOR FILING DATE: 1999-11-02  
; PRIOR APPLICATION NUMBER: 09/704,036  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/203,349  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 1252  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-012-762-20

Query Match 9.5%; Score 67; DB 4; Length 1252;  
Best Local Similarity 34.7%; Pred. No. 1.4e+02;  
Matches 17; Conservative 10; Mismatches 20; Indels 2; Gaps 2;

QY 84 LYLALDLYVFPQISSVVKDR-KKAVLSDIGVSGEPHPAGTPTCTESTGCPG 131

DB 277 IYAKLEYNPG-GSIKDRIAKSMVEAEASGRHPSRSTLIPTSGNTG 324

```

RESULT 45
US-09-519-232-74
; Sequence 74, Application US/09519232
; Patent No. 6528702
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RT2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-519-232-74

Query Match          9.5%; Score 66.5; DB 4; Length 369;
Best Local Similarity 24.2%; Pred. No. 31;
Matches 30; Conservative 19; Mismatches 42; Indels 33; Gaps 5;

QY 5 AYGAGKAGGADPDTLVROQHTILRVVSMFLSIWFGSIVNEGYLNSASGEQFCI----60
Db 32 AYGSGTSGSSYEIISLKSNNLEQLLSDSSDFTDAEIVVEG-----VSLGVHRCILAAR 87
QY 61 -----YNNRPNACS-----YGVAVGVLAFLTCLLYL---ALDVPFPQIS 96
Db 88 SKFFQDLFRKEKSCGKEGPRYSMTDILPYG-KVGVEAFVTLSYLSKLGKHPPEVS 146
QY 97 SVKD 100
Db 147 TCMD 150

RESULT 46
US-09-441-411-8
; Sequence 8, Application US/09441411
; Patent No. 6734172
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-441-411-8

Query Match          9.5%; Score 66.5; DB 4; Length 378;
Best Local Similarity 23.0%; Pred. No. 32;
Matches 29; Conservative 22; Mismatches 44; Indels 31; Gaps 7;

QY 4 GAY---GAGKAGGA--FDPTLVLRQP-----HTILRVVSMFLS---IVV-----FG 41
Db 133 GSYSGIGAGMTAAIGDYRVNVTKPMNRNMTFTKAVIMNIIWLYCTPWWVLPTQFWD 192
QY 42 SIVNEGYLNSASGEQFCIYNNRPNACSIVGAVGVLAFLT---CLLYLALDVPFPQISSVK 99
Db 193 RFVPEGYLTS-----CSFDYLSDNFTRLVGTFTIFFSPVCPMTLMILYYISQIVGHVF 245
QY 100 DRKAV 105
; :||:

RESULT 47
US-09-489-039A-9365
; Sequence 9365, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9365
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9365

Query Match          9.4%; Score 66; DB 4; Length 237;
Best Local Similarity 23.4%; Pred. No. 20;
Matches 25; Conservative 20; Mismatches 32; Indels 30; Gaps 4;

QY 13 GAFDPVTLV--RQPHITLWVSWLFSI-----VVFGSIVNEGYL 49
Db 107 GFYSLSLVFRQHQWKSRLVALIFAIAWIVLGLSFVWVPLNGWSSLAIFGLFLVLGGI 166
QY 50 NSAGEGEQFCIYNNRPNACSIVGAVGVLAFLTCLLYLALDVPFPQIS 96
Db 167 SRVNGCQ---TRKQSGAGWNIFIGLLDLIIACLWLAWN---PQOS 206

RESULT 48
US-09-090-567-2
; Sequence 2, Application US/09090567
; Patent No. 5989549
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Robert
; APPLICANT: Brub, Bruno
; APPLICANT: Lgar, Christine
; APPLICANT: Gaudreault, Christian
; TITLE OF INVENTION: Acrosomal Sperm Protein And
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swabey Ogilvy Renault
; STREET: 1600 - 1981 McGill College
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Kevin P
; REGISTRATION NUMBER: 26,674
; REFERENCE/DOCKET NUMBER: 13045-2"US" FC/CC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514-845-7126
```

```
/ TELEFAX: 514-288-8389
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 244 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
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US-09-090-567-2
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    Best Local Similarity 25.2%; Pred. No. 20;
    Matches 26; Conservative 16; Mismatches 43; Indels 18; Gaps 4;

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Db 110 SVLQV-----SQVAKGMIRGVAGSIVNISSVAVVTFPGLATYSSTKGAITMLTKAMA 164

QY 86 LALDVYFPQISSVKDRKKAVLSDIG--VSSEP-----HP 117
Db 165 MELGPYKIRVNSV--NPTVLTDMGKKVSADPEFAKKLKERHP 205

RESULT 49
US-08-118-270-10
/ Sequence 10, Application US/08118270
/ Patent No. 5508384
/ GENERAL INFORMATION:
/ APPLICANT: Murphy, Randall B.
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY-2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 317 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-118-270-10
    Query Match          9.4%; Score 66; DB 1; Length 317;
    Best Local Similarity 22.5%; Pred. No. 29;
    Matches 27; Conservative 24; Mismatches 43; Indels 26; Gaps 5;

QY 26 TLIRVSVWLFISIVFGSIVNEGYNLSAGEQECIYNRPNACSYGVAVGVLAFLTCLLY 85
Db 110 SVLQV-----SQVAKGMIRGVAGSIVNISSVAVVTFPGLATYSSTKGAITMLTKAMA 164

QY 86 LALDVYFPQISSVKDRKKAVLSDIG--VSSEP-----HP 117
Db 165 MELGPYKIRVNSV--NPTVLTDMGKKVSADPEFAKKLKERHP 205

RESULT 49
US-08-118-270-10
/ Sequence 10, Application US/08118270
/ Patent No. 5508384
/ GENERAL INFORMATION:
/ APPLICANT: Murphy, Randall B.
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY-2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 317 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-118-270-10
    Query Match          9.4%; Score 66; DB 1; Length 317;
    Best Local Similarity 22.5%; Pred. No. 29;
    Matches 27; Conservative 24; Mismatches 43; Indels 26; Gaps 5;
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QY 14 AFDPTLVLRQPH-----ILRVSVWLFISIVFGSIVNEGYNLSASEG 55
Db 85 SFDYFCVTKPLTYPVKRTTKMAGMIAAAVLSFILWAPALFWQFIVG---VRTVEDG 141
QY 56 EQFCIYNRPNACSYGVAVGVLAFLTCLLYLALDVYFPQISS---VKDRKKAVLSDIGVS 112
Db 142 ECVIOFFSNP-AVTFTGTAIAAF-YLPVIIMIVLYWHISRASKSRIRKKOKPEPVANQDPVS 199

RESULT 50
PCT-US93-08528-10
/ Sequence 10, Application PC/TUS9308528
/ GENERAL INFORMATION:
/ APPLICANT: New York University
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/08528
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 317 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
PCT-US93-08528-10
    Query Match          9.4%; Score 66; DB 5; Length 317;
    Best Local Similarity 22.5%; Pred. No. 29;
    Matches 27; Conservative 24; Mismatches 43; Indels 26; Gaps 5;

QY 14 AFDPTLVLRQPH-----ILRVSVWLFISIVFGSIVNEGYNLSASEG 55
Db 85 SFDYFCVTKPLTYPVKRTTKMAGMIAAAVLSFILWAPALFWQFIVG---VRTVEDG 141
QY 56 EQFCIYNRPNACSYGVAVGVLAFLTCLLYLALDVYFPQISS---VKDRKKAVLSDIGVS 112
Db 142 ECVIOFFSNP-AVTFTGTAIAAF-YLPVIIMIVLYWHISRASKSRIRKKOKPEPVANQDPVS 199

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:54 ; Search time 60 seconds  
(without alignments)  
859.837 Million cell updates/sec

Title: US-10-643-836-297  
Perfect score: 703  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1755696 seqs, 390834859 residues 1755696

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Listing first 50 summaries

Database : Published Applications AA.\*

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- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pdb.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	703	100.0	132	10	US-09-876-997-297
3	703	100.0	132	17	US-10-643-836-297
4	296	42.1	224	9	US-09-788-295A-162
5	296	42.1	224	9	US-09-788-697-162
6	296	42.1	224	9	US-09-788-192A-162
7	296	42.1	224	9	US-09-999-832A-162
8	296	42.1	224	10	US-09-978-189-162
9	296	42.1	224	10	US-09-978-608A-162
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24	296	42.1	224	10	US-09-978-643A-162
25	296	42.1	224	10	US-09-978-375A-162
26	296	42.1	224	10	US-09-978-298A-162
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28	296	42.1	224	10	US-09-978-681A-162
29	296	42.1	224	10	US-09-978-194A-162
30	296	42.1	224	10	US-09-999-829A-162
31	296	42.1	224	10	US-09-978-299A-162
32	296	42.1	224	10	US-09-978-544A-162
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34	296	42.1	224	11	US-09-978-802A-162
35	296	42.1	224	11	US-09-999-831A-162
36	296	42.1	224	12	US-09-978-824-162
37	296	42.1	224	14	US-10-017-081A-162
38	296	42.1	224	14	US-10-167-749-162
39	296	42.1	224	14	US-10-013-921A-162
40	296	42.1	224	14	US-10-016-177A-162
41	296	42.1	224	14	US-10-166-709A-162
42	296	42.1	224	14	US-10-143-031A-162
43	296	42.1	224	14	US-10-143-030A-162
44	296	42.1	224	14	US-10-002-967A-162
45	296	42.1	224	14	US-10-017-083A-162
46	296	42.1	224	14	US-10-145-128A-162
47	296	42.1	224	14	US-10-017-191A-162
48	296	42.1	224	14	US-10-143-028A-162
49	296	42.1	224	14	US-10-143-029A-162
50	296	42.1	224	14	US-10-143-029A-162

ALIGNMENTS

RESULT 1  
US-09-731-872-297  
; Sequence 297, Application US/09731872  
; Patent No. US20020102604A1  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Bouqueloret, Lydie  
; APPLICANT: Jobert, Severin  
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS  
; FILE REFERENCE: 78.053.REG  
; CURRENT APPLICATION NUMBER: US/09/731,872  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,629  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: US 60/187,470  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 482  
; SOFTWARE: Patent.pm  
; SEQ ID NO 297  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -41..-1  
US-09-731-872-297

Query Match 100.0%; Score 703; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 4.3e-73;

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Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEGGAYGAGKAGAGDPYTLVRQPHHTILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVSGEPHPACT 120
Db 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVSGEPHPACT 120
QY 121 PCTESTEGCGP 132
Db 121 PCTESTEGCGP 132

RESULT 2
US-09-876-997-297
; Sequence 297, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 297
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41...-1
US-09-876-997-297

Query Match 100.0%; Score 703; DB 10; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGAGDPYTLVRQPHHTILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
Db 1 MEGGAYGAGKAGAGDPYTLVRQPHHTILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVSGEPHPACT 120
Db 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVSGEPHPACT 120
QY 121 PCTESTEGCGP 132
Db 121 PCTESTEGCGP 132

RESULT 3
US-10-643-836-297
; Sequence 297, Application US/10643836
; Publication No. US20050096458A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/10/643,836
; CURRENT FILING DATE: 2003-08-19
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; PRIOR APPLICATION NUMBER: US/09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 297
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41...-1
US-10-643-836-297

Query Match 100.0%; Score 703; DB 17; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEGGAYGAGKAGAGDPYTLVRQPHHTILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
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Db 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVSGEPHPACT 120
QY 121 PCTESTEGCGP 132
Db 121 PCTESTEGCGP 132

RESULT 4
US-09-978-295A-162
; Sequence 162, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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6	PRIOR FILING DATE: 1997-11-13	6	PRIOR APPLICATION NUMBER: 60/081819
7	PRIOR APPLICATION NUMBER: 60/066364	7	PRIOR FILING DATE: 1998-04-15
8	PRIOR FILING DATE: 1997-11-21	8	PRIOR APPLICATION NUMBER: 60/081952
9	PRIOR APPLICATION NUMBER: 60/077450	9	PRIOR FILING DATE: 1998-04-15
10	PRIOR FILING DATE: 1998-03-10	10	PRIOR APPLICATION NUMBER: 60/081838
11	PRIOR APPLICATION NUMBER: 60/077632	11	PRIOR FILING DATE: 1998-04-15
12	PRIOR FILING DATE: 1998-03-11	12	PRIOR APPLICATION NUMBER: 60/082568
13	PRIOR APPLICATION NUMBER: 60/077641	13	PRIOR FILING DATE: 1998-04-21
14	PRIOR FILING DATE: 1998-03-11	14	PRIOR APPLICATION NUMBER: 60/082569
15	PRIOR APPLICATION NUMBER: 60/077649	15	PRIOR FILING DATE: 1998-04-21
16	PRIOR FILING DATE: 1998-03-11	16	PRIOR APPLICATION NUMBER: 60/082704
17	PRIOR APPLICATION NUMBER: 60/077791	17	PRIOR FILING DATE: 1998-04-22
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19	PRIOR APPLICATION NUMBER: 60/078004	19	PRIOR FILING DATE: 1998-04-22
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35	PRIOR APPLICATION NUMBER: 60/079689	35	PRIOR FILING DATE: 1998-04-29
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38	PRIOR FILING DATE: 1998-03-27	38	PRIOR APPLICATION NUMBER: 60/083554
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43	PRIOR APPLICATION NUMBER: 60/079920	43	PRIOR FILING DATE: 1998-04-29
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47	PRIOR APPLICATION NUMBER: 60/080105	47	PRIOR FILING DATE: 1998-04-30
48	PRIOR FILING DATE: 1998-03-31	48	PRIOR APPLICATION NUMBER: 60/084366
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60	PRIOR FILING DATE: 1998-04-01	60	PRIOR APPLICATION NUMBER: 60/084598
61	PRIOR APPLICATION NUMBER: 60/080334	61	PRIOR FILING DATE: 1998-05-07
62	PRIOR FILING DATE: 1998-04-01	62	PRIOR APPLICATION NUMBER: 60/084600
63	PRIOR APPLICATION NUMBER: 60/081070	63	PRIOR FILING DATE: 1998-05-07
64	PRIOR FILING DATE: 1998-04-08	64	PRIOR APPLICATION NUMBER: 60/084627
65	PRIOR APPLICATION NUMBER: 60/081049	65	PRIOR FILING DATE: 1998-05-07
66	PRIOR FILING DATE: 1998-04-08	66	PRIOR APPLICATION NUMBER: 60/084643
67	PRIOR APPLICATION NUMBER: 60/081071	67	PRIOR FILING DATE: 1998-05-07
68	PRIOR FILING DATE: 199		





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2 PRIOR FILING DATE: 1998-04-15  
3 PRIOR APPLICATION NUMBER: 60/081819  
4 PRIOR FILING DATE: 1998-04-15  
5 PRIOR APPLICATION NUMBER: 60/081952  
6 PRIOR FILING DATE: 1998-04-15  
7 PRIOR APPLICATION NUMBER: 60/081838  
8 PRIOR FILING DATE: 1998-04-15  
9 PRIOR APPLICATION NUMBER: 60/082568  
10 PRIOR FILING DATE: 1998-04-21  
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12 PRIOR FILING DATE: 1998-04-21  
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16 PRIOR FILING DATE: 1998-04-22  
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18 PRIOR FILING DATE: 1998-04-22  
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35 PRIOR APPLICATION NUMBER: 60/083545  
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41 PRIOR APPLICATION NUMBER: 60/083559  
42 PRIOR FILING DATE: 1998-04-29  
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44 PRIOR FILING DATE: 1998-04-29  
45 PRIOR APPLICATION NUMBER: 60/083742  
46 PRIOR FILING DATE: 1998-04-30  
47 PRIOR APPLICATION NUMBER: 60/084366  
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49 PRIOR APPLICATION NUMBER: 60/084414  
50 PRIOR FILING DATE: 1998-05-06  
51 PRIOR APPLICATION NUMBER: 60/084441  
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56 PRIOR FILING DATE: 1998-05-07  
57 PRIOR APPLICATION NUMBER: 60/084640  
58 PRIOR FILING DATE: 1998-05-07  
59 PRIOR APPLICATION NUMBER: 60/084598  
60 PRIOR FILING DATE: 1998-05-07  
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65 PRIOR APPLICATION NUMBER: 60/084643  
66 PRIOR FILING DATE: 1998-05-07  
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69 PRIOR APPLICATION NUMBER: 60/085338  
70 PRIOR FILING DATE: 1998-05-13  
71 PRIOR APPLICATION NUMBER: 60/085323  
72 PRIOR FILING DATE: 1998-05-13  
73 PRIOR APPLICATION NUMBER: 60/085582

1 PRIOR FILING DATE: 1998-05-15  
2 PRIOR APPLICATION NUMBER: 60/085700  
3 PRIOR FILING DATE: 1998-05-15  
4 PRIOR APPLICATION NUMBER: 60/085689  
5 PRIOR FILING DATE: 1998-05-15  
6 PRIOR APPLICATION NUMBER: 60/085579  
7 PRIOR FILING DATE: 1998-05-15  
8 PRIOR APPLICATION NUMBER: 60/085580  
9 PRIOR FILING DATE: 1998-05-15  
10 PRIOR APPLICATION NUMBER: 60/085573  
11 PRIOR FILING DATE: 1998-05-15  
12 PRIOR APPLICATION NUMBER: 60/085704  
13 PRIOR FILING DATE: 1998-05-15  
14 PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 9; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;  
QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNCGYLNLSAGEQFCI 60  
Db 1 MESGAYGAKAGGSGDLRRFLTQPVVARAVCLVFALIVFCIYGGYNAHESKQMYCV 60  
QY 61 YNRNPACSYGVAVGVLAFLTCLLLVLDVFPQISSVKDKKAVLSDI 109  
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVLVIGDL 109

RESULT 6  
US-09-978-192A-162  
Sequence 162, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13



; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15

Query Match 42.1%; Score 296; DB 9; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGAFDPYTLVQPHITLIRVSWLSIVVFGSIVNEGYNLSASEGEQFCI 60
DB 1 MESGAYGAKAGSGFDLRRFLTQPVQVARAVCLVFLALIVFCIYGEYSNAHESKQMYCV 60

QY 61 YNRNPACSYGVANGVLAELTCLLLALDQVYFPQISSVKDKKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLLVDVDFPQISNATDRKYLVIIGDL 109

RESULT 7
US-09-999-832A-162
; Sequence 162, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15

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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 9; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAKGAGAPDPTLVROPHITLIRVSWLPSIVVFGSIVNEGYNLSASEGQFCI 60  
DB 1 MESGAYGAAGAGGSFDLRRFLTPQVVARAVCLVFLALIVFSCIYGEYSNAHESKOMYCV 60  
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVPFQISSVVDKKAVLSDI 109  
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDVDFPQISNATDRKYLVLIGDL 109

## RESULT 8

US-09-978-189-162  
; Sequence 162, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1997-11-03  
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; PRIOR FILING DATE: 1998-03-11

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PRIOR FILING DATE:	1998-03-12
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PRIOR APPLICATION NUMBER:	60/078939
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PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079920
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PRIOR FILING DATE:	1998-03-30
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PRIOR APPLICATION NUMBER:	60/081952
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081838
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568

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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
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Db 1 MESSGAYGAAGKAGGSDLRRLFTQPVVARAVCLVFLVFCIYGEYSNAHESKQMYCV 60

QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVTGDL 109

RESULT 9
US-09-978-608A-162
; Sequence 162, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens

Query Match      42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MESSGAYGAAGKAGGSDLRRLFTQPVVARAVCLVFLVFCIYGEYSNAHESKQMYCV 60

QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVTGDL 109
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Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVTGDL 109

RESULT 10
US-09-978-585A-162
; Sequence 162, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens

Query Match      42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MESSGAYGAAGKAGGSDLRRLFTQPVVARAVCLVFLVFCIYGEYSNAHESKQMYCV 60

QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
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Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVTGDL 109

RESULT 11
US-09-978-191A-162
; Sequence 162, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
```

APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kiljavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630PIC4  
 CURRENT APPLICATION NUMBER: US/09/978,191A  
 CURRENT FILING DATE: 2001-10-15  
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; PRIOR APPLICATION NUMBER: 60/084414  
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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;

Best Local Similarity 48.6%; Pred. No. 1.2e-25;

Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAGDPYTLVROPHILRVVSWLFSIVVFGSIVNBSYLNLSASEGEOFCI 60

Db 1 MESSGAYGAAGKAGGSGDLRRFLTPQVAVRAVCLVAFALVFSCTIYGEGYSNAHESKOMYCV 60

QY 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDI 109

Db 61 FNRNEDACRYGSAIGVLAFLASAFFLLVVDVAYFPQISNATDRKYLVIIGDL 109

RESULT 13

US-09-978-564A-162

; Sequence 162, Application US/09978564A

; Publication No. US20030050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C25  
CURRENT APPLICATION NUMBER: US/09/978,564A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918595  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05

[illegible]



APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
CURRENT FILING DATE: 2001-10-16  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;

Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGAYGAGKAGGADPYTLVRPHITLRSVWLFPSIVVFGSTVNEGYLNSASEGQFCI 60  
DB 1 MEGAYGAGKAGGSDLRFLTPQVVARAVCLVFLVFCIYGGYNAHESKOMYCV 60  
QY 61 YNRNPNACSYGVAVGVLAFELTCLLYLALDVYFPQISSVKDRKKAFLSDI 109  
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVLGDL 109

RESULT 16

US-09-978-824-162  
Sequence 162, Application US/09978824  
Publication No. US20030055216A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.

;  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC14  
; CURRENT APPLICATION NUMBER: US/09/978,824  
; CURRENT FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
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61	PRIOR APPLICATION NUMBER: 60/084441
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63	PRIOR APPLICATION NUMBER: 60/084637
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65	PRIOR APPLICATION NUMBER: 60/084639
66	PRIOR FILING DATE: 1998-05-07
67	PRIOR APPLICATION NUMBER: 60/084640

1	PRIOR FILING DATE: 1998-05-07	
2	PRIOR APPLICATION NUMBER: 60/084598	
3	PRIOR FILING DATE: 1998-05-07	
4	PRIOR APPLICATION NUMBER: 60/084600	
5	PRIOR FILING DATE: 1998-5-07	
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14	PRIOR APPLICATION NUMBER: 60/085323	
15	PRIOR FILING DATE: 1998-05-13	
16	PRIOR APPLICATION NUMBER: 60/085582	
17	PRIOR FILING DATE: 1998-05-15	
18	PRIOR APPLICATION NUMBER: 60/085700	
19	PRIOR FILING DATE: 1998-05-15	
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22	PRIOR APPLICATION NUMBER: 60/085579	
23	PRIOR FILING DATE: 1998-05-15	
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26	PRIOR APPLICATION NUMBER: 60/085573	
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28	PRIOR APPLICATION NUMBER: 60/085704	
29	PRIOR FILING DATE: 1998-05-15	
30	PRIOR APPLICATION NUMBER: 60/085697	

Query Match	42.1%;	Score 296;	DB 10;	Length 224;
Best Local Similarity	48.6%;	Pred. No. 1.2e-25;		
Matches 53: Conservative	19;	Mismatches 37;	Indels 0;	

Qy	1	MEGGAYGAGKACGADPDTYLRPHPTIILRVVSWLFSLVVFSGIVNEGYLNSAEGEQPCI	60
Db	1	MEGGAYGAGKACGADPDTYLRPHPTIILRVVSWLFSLVVFSGIVNEGYLNSAEGEQPCI	60
Qy	61	YNRNPNCASYGAVAGVLAFLTCLLYLALDVPFPQISSVKRDKKAVLSDI	109
Db	61	YNRNPNCASYGAVAGVLAFLTCLLYLALDVPFPQISSVKRDKKAVLSDI	109

RESULT 17  
US-09-918-585A-162  
; Sequence 162, Application US/09918585A  
; Publication No. US20030060406A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Destoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C1  
CURRENT APPLICATION NUMBER: US/09/918,585A  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;

Best Local Similarity 48.6%; Pred. No. 1.2e-25; Mismatches 37; Indels 0; Gaps 0;

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Db 1 MESGAYGAAGKAGGSFDLRFLTPQVVARAVCLVFLVFCIYGEYSNAHESKQMYCV 60

QY 61 YNRNPACSYGVAVGVGLAFLTLCLLYALDVPFPQISSVKDRKKAVLSOI 109

Db 61 FNRNEDACRYGSAIGVLAFLASAPFLVVDVAYFPQISNATDRKYLVTIGDL 109

RESULT 19

US-09-978-423A-162

; Sequence 162, Application US/09978423A

; Publication No. US20030069178A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC21

1 ; CURRENT APPLICATION NUMBER: US/09/978,423A  
2 ; CURRENT FILING DATE: 2002-05-16  
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4 ; PRIOR FILING DATE: 2001-07-30  
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAGCAGCAGGAFDPTLVROPHILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
DB 1 MESSGAGCAKAGGSGFDRRLFTQPVVARAVCLVFAIVFCISYGGSGNAHESKOMYCV 60

QY 61 YNRNPACSVGAVGVLFATLLCLYLDVYFPQISSVKDRKKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASFFLVVDAYFPQISNATDRKYLVIQDL 109

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; Sequence 162, Application US/09978193A
; Publication No. US20030073624A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC6
; CURRENT APPLICATION NUMBER: US/09/978,193A
; CURRENT FILING DATE: 2002-02-21
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; PRIOR APPLICATION NUMBER: 60/062250
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; Sequence 162, Application US/09999830A
; Publication No. US20030077000A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertszen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shetton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmitted
; FILE REFERENCE: P2630P1C70
; CURRENT APPLICATION NUMBER: US/09/999
; CURRENT FILING DATE: 2001-08-31
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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52	PRIOR FILING DATE: 1998-03-31	
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54	PRIOR FILING DATE: 1998-04-01	
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63	PRIOR APPLICATION NUMBER: 60/081049	
64	PRIOR FILING DATE: 1998-04-08	
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66	PRIOR FILING DATE: 1998-04-08	
67	PRIOR APPLICATION NUMBER: 60/081195	
68	PRIOR FILING DATE: 1998-04-08	
69	PRIOR APPLICATION NUMBER: 60/081203	
70	PRIOR FILING DATE: 1998-04-09	
71	PRIOR APPLICATION NUMBER: 60/081229	
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56	PRIOR APPLICATION NUMBER: 60/084639		
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61	PRIOR FILING DATE: 1998-05-07	60/084643	
62	PRIOR APPLICATION NUMBER: 60/084643		
63	PRIOR FILING DATE: 1998-05-07	60/085339	
64	PRIOR APPLICATION NUMBER: 60/085339		
65	PRIOR FILING DATE: 1998-05-13	60/085338	
66	PRIOR APPLICATION NUMBER: 60/085338		
67	PRIOR FILING DATE: 1998-05-13	60/085323	
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDYTLVROPHTILRVVSMFLSVVFGSIWVNEGYLNSASEGQFCI 60
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QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDKKAVLSDI 109
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Db 61 FNRNEDACRYGSAIGVLAFSLASAFFLVVDAYFPQISNATDKYLVIGDL 109
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RESULT 22
US-09-978-757A-162
; Sequence 162, Application US/09978757A
; Publication No. US20030083248A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C26
; CURRENT APPLICATION NUMBER: US/09/978.757A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match          42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps

Qy 1 MEGGAYGAGKAGADPYTLVRQPHILRVVSWLFSIVVFGSIVNEGYLNSASEGEQFCI 60
Db 1 MMSGYGAAGAKSGSFDLRRFLTPQPVARAVCLVFALIVFSCIVGEGYSNAHESKQMYCV 60

Qy 61 YNRNPACSYGVAVGVIAFLTCLLLYLDVYFPQISSVKDKKAVLSPI 109
Db 61 FNRNDAKCYGAIGVIAFLASAFVVDVYFPQISNATDRKYLVIQDL 109

RESULT 23
US-09-978-187B-162
; Sequence 162, Application US/09978187B
; Publication No. US20030096744A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCES: P2630PIC5
; CURRENT APPLICATION NUMBER: US/09/978,187B
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21

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[illegible]



APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC2  
CURRENT APPLICATION NUMBER: US/09/978,298A  
CURRENT FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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Query Match 42.1%; Score 296; DB 10; Length 224;  
 Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
 Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGACAGCAGGAFDYTLVROPHILRWVSLFVVGSTVNRGYNLSASEGQFCI 60  
 DB 1 MEGGAYGAAGAGGFDLRLFTOPQVVARACLVFALIVFSCYIGGYNASHESKOMYCV 60  
 QY 61 YNRPNACSYGVAVGVLAFTCLLYLALDVYFPQISSVKDKKAVLSDI 109  
 DB 61 FNRNEDACRYSAGVLAFLASAFFLWDAFFQISNATDRKLVIGDL 109

RESULT 27  
 US-09-978-188A-162  
 ; Sequence 162, Application US/09978188A  
 ; Publication No. US20030139328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C8  
 ; CURRENT APPLICATION NUMBER: US/09/978,188A  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGADPYTLVROPHTILRWVWLSFIVVFGSIVNVEGYLNSASEGEQFCI 60  
Db 1 MESSGAYGAAGAGGSGFDRFLPTQPVVARAVCLVFLVFPSCIYGEQYSHAKSKQMYCV 60  
QY 61 YNRPNACSYGVAVGVLAFITCLLYLALDVFYFQISSVKDKKXVLSDI 109  
Db 61 FNEEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDKYLVIGDL 109

RESULT 28  
US-09-978-681A-162  
; Sequence 162, Application US/09978681A  
; Publication No. US20030195148A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC18  
CURRENT APPLICATION NUMBER: US/09/978,681A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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7	PRIOR APPLICATION NUMBER: 60/083742	
7	PRIOR FILING DATE: 1998-04-30	
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RESULT 29
US-09-978-194A-162
; Sequence 162, Application US/09978194A
; Publication No. US20030195333A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

```

1 APPLICANT: Goddard, Audrey  
 2 APPLICANT: Godowski, Paul J.  
 3 APPLICANT: Grimaldi, J. Christopher  
 4 APPLICANT: Gurney, Austin L.  
 5 APPLICANT: Hillan, Kenneth J.  
 6 APPLICANT: Kljavin, Ivar J.  
 7 APPLICANT: Kuo, Sophia S.  
 8 APPLICANT: Napier, Mary A.  
 9 APPLICANT: Pan, James;  
 10 APPLICANT: Paoni, Nicholas P.  
 11 APPLICANT: Roy, Margaret Ann  
 12 APPLICANT: Shelton, David L.  
 13 APPLICANT: Stewart, Timothy A.  
 14 APPLICANT: Tumas, Daniel  
 15 APPLICANT: Williams, P. Mickey  
 16 APPLICANT: Wood, William I.  
 17 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 18 TITLE OF INVENTION: Acids Encoding the Same  
 19 FILE REFERENCE: P2630PlC10  
 20 CURRENT APPLICATION NUMBER: US/09/978,194A  
 21 CURRENT FILING DATE: 2001-10-15  
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 23 PRIOR FILING DATE: 2001-07-30  
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 71 PRIOR FILING DATE: 1998-03-30  
 72 PRIOR APPLICATION NUMBER: 60/080105  
 73 PRIOR FILING DATE: 1998-03-31  
 74 PRIOR APPLICATION NUMBER: 60/080107  
 75 PRIOR FILING DATE: 1998-03-31









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; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGADPPYTLVROPHTILRVSWLFSIVVFGSTVNEGYNLSASEGGEQFCI 60
Db 1 MESGAYGAAGAGGSFDRFLTPQVVARAVCLVFLVIFSCYIGGYNASHESKOMYCV 60

QY 61 YNPNACSGVAGVGLAFVLTCLLYLALDVFYFQISSVKDRKKAVLSDI 109
Db 61 FNEDEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKVLVIGDL 109

RESULT 33
US-09-978-665A-162
; Sequence 162, Application US/09978665A
; Publication No. US20030199437A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C19
; CURRENT APPLICATION NUMBER: US/09/978, 665A
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; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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1	PRIOR APPLICATION NUMBER: 60/065311	2	PRIOR FILING DATE: 1998-04-15
2	PRIOR FILING DATE: 1997-11-13	3	PRIOR APPLICATION NUMBER: 60/081819
3	PRIOR APPLICATION NUMBER: 60/066364	4	PRIOR FILING DATE: 1998-04-15
4	PRIOR FILING DATE: 1997-11-21	5	PRIOR APPLICATION NUMBER: 60/081952
5	PRIOR APPLICATION NUMBER: 60/077450	6	PRIOR FILING DATE: 1998-04-15
6	PRIOR FILING DATE: 1998-03-10	7	PRIOR APPLICATION NUMBER: 60/081838
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8	PRIOR FILING DATE: 1998-03-11	9	PRIOR APPLICATION NUMBER: 60/082568
9	PRIOR APPLICATION NUMBER: 60/077641	10	PRIOR FILING DATE: 1998-04-21
10	PRIOR FILING DATE: 1998-03-11	11	PRIOR APPLICATION NUMBER: 60/082569
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12	PRIOR FILING DATE: 1998-03-11	13	PRIOR APPLICATION NUMBER: 60/082704
13	PRIOR APPLICATION NUMBER: 60/077791	14	PRIOR FILING DATE: 1998-04-22
14	PRIOR FILING DATE: 1998-03-12	15	PRIOR APPLICATION NUMBER: 60/082804
15	PRIOR APPLICATION NUMBER: 60/078004	16	PRIOR FILING DATE: 1998-04-22
16	PRIOR FILING DATE: 1998-03-13	17	PRIOR APPLICATION NUMBER: 60/082700
17	PRIOR APPLICATION NUMBER: 60/078886	18	PRIOR FILING DATE: 1998-04-22
18	PRIOR FILING DATE: 1998-03-20	19	PRIOR APPLICATION NUMBER: 60/082797
19	PRIOR APPLICATION NUMBER: 60/078936	20	PRIOR FILING DATE: 1998-04-22
20	PRIOR FILING DATE: 1998-03-20	21	PRIOR APPLICATION NUMBER: 60/082796
21	PRIOR APPLICATION NUMBER: 60/078910	22	PRIOR FILING DATE: 1998-04-23
22	PRIOR FILING DATE: 1998-03-20	23	PRIOR APPLICATION NUMBER: 60/083336
23	PRIOR APPLICATION NUMBER: 60/078939	24	PRIOR FILING DATE: 1998-04-27
24	PRIOR FILING DATE: 1998-03-20	25	PRIOR APPLICATION NUMBER: 60/083322
25	PRIOR APPLICATION NUMBER: 60/079294	26	PRIOR FILING DATE: 1998-04-28
26	PRIOR FILING DATE: 1998-03-25	27	PRIOR APPLICATION NUMBER: 60/083392
27	PRIOR APPLICATION NUMBER: 60/079656	28	PRIOR FILING DATE: 1998-04-29
28	PRIOR FILING DATE: 1998-03-26	29	PRIOR APPLICATION NUMBER: 60/083495
29	PRIOR APPLICATION NUMBER: 60/079664	30	PRIOR FILING DATE: 1998-04-29
30	PRIOR FILING DATE: 1998-03-27	31	PRIOR APPLICATION NUMBER: 60/083496
31	PRIOR APPLICATION NUMBER: 60/079689	32	PRIOR FILING DATE: 1998-04-29
32	PRIOR FILING DATE: 1998-03-27	33	PRIOR APPLICATION NUMBER: 60/083499
33	PRIOR APPLICATION NUMBER: 60/079663	34	PRIOR FILING DATE: 1998-04-29
34	PRIOR FILING DATE: 1998-03-27	35	PRIOR APPLICATION NUMBER: 60/083545
35	PRIOR APPLICATION NUMBER: 60/079728	36	PRIOR FILING DATE: 1998-04-29
36	PRIOR FILING DATE: 1998-03-27	37	PRIOR APPLICATION NUMBER: 60/083554
37	PRIOR APPLICATION NUMBER: 60/079786	38	PRIOR FILING DATE: 1998-04-29
38	PRIOR FILING DATE: 1998-03-27	39	PRIOR APPLICATION NUMBER: 60/083558
39	PRIOR APPLICATION NUMBER: 60/079920	40	PRIOR FILING DATE: 1998-04-29
40	PRIOR FILING DATE: 1998-03-30	41	PRIOR APPLICATION NUMBER: 60/083559
41	PRIOR APPLICATION NUMBER: 60/079923	42	PRIOR FILING DATE: 1998-04-29
42	PRIOR FILING DATE: 1998-03-30	43	PRIOR APPLICATION NUMBER: 60/083500
43	PRIOR APPLICATION NUMBER: 60/080105	44	PRIOR FILING DATE: 1998-04-29
44	PRIOR FILING DATE: 1998-03-31	45	PRIOR APPLICATION NUMBER: 60/083742
45	PRIOR APPLICATION NUMBER: 60/080107	46	PRIOR FILING DATE: 1998-04-30
46	PRIOR FILING DATE: 1998-03-31	47	PRIOR APPLICATION NUMBER: 60/084366
47	PRIOR APPLICATION NUMBER: 60/080165	48	PRIOR FILING DATE: 1998-05-05
48	PRIOR FILING DATE: 1998-03-31	49	PRIOR APPLICATION NUMBER: 60/084414
49	PRIOR APPLICATION NUMBER: 60/080194	50	PRIOR FILING DATE: 1998-05-06
50	PRIOR FILING DATE: 1998-03-31	51	PRIOR APPLICATION NUMBER: 60/084441
51	PRIOR APPLICATION NUMBER: 60/080327	52	PRIOR FILING DATE: 1998-05-06
52	PRIOR FILING DATE: 1998-04-01	53	PRIOR APPLICATION NUMBER: 60/084637
53	PRIOR APPLICATION NUMBER: 60/080328	54	PRIOR FILING DATE: 1998-05-07
54	PRIOR FILING DATE: 1998-04-01	55	PRIOR APPLICATION NUMBER: 60/084639
55	PRIOR APPLICATION NUMBER: 60/080333	56	PRIOR FILING DATE: 1998-05-07
56	PRIOR FILING DATE: 1998-04-01	57	PRIOR APPLICATION NUMBER: 60/084640
57	PRIOR APPLICATION NUMBER: 60/080334	58	PRIOR FILING DATE: 1998-05-07
58	PRIOR FILING DATE: 1998-04-01	59	PRIOR APPLICATION NUMBER: 60/084598
59	PRIOR APPLICATION NUMBER: 60/081070	60	PRIOR FILING DATE: 1998-05-07
60	PRIOR FILING DATE: 1998-04-08	61	PRIOR APPLICATION NUMBER: 60/084600
61	PRIOR APPLICATION NUMBER: 60/081049	62	PRIOR FILING DATE: 1998-05-07
62	PRIOR FILING DATE: 1998-04-08	63	PRIOR APPLICATION NUMBER: 60/084627
63	PRIOR APPLICATION NUMBER: 60/081071	64	PRIOR FILING DATE: 1998-05-07
64	PRIOR FILING DATE: 1998-04-08	65	PRIOR APPLICATION NUMBER: 60/084643
65	PRIOR APPLICATION NUMBER: 60/081195	66	PRIOR FILING DATE: 1998-05-07
66	PRIOR FILING DATE: 1998-04-08	67	PRIOR APPLICATION NUMBER: 60/085339
67	PRIOR APPLICATION NUMBER: 60/081203	68	PRIOR FILING DATE: 1998-05-13
68	PRIOR FILING DATE: 1998-04-09	69	PRIOR APPLICATION NUMBER: 60/085338
69	PRIOR APPLICATION NUMBER: 60/081229		

;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;  
Best Local Similarity 48.8%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;  
  
QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVVSFLFVSGIVNFGYLSASEGEQFCI 60  
Db 1 MEGGAYGAGKAGGAFDLRRFLTPQVVARAVCLVFLVFSCLYGGYNAHESKQMYCV 60  
  
QY 61 YNRPNACSYGVAVGLAFITLCLLYALDVPFQISSVKDKKAVLSDI 109  
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDVDFYFQISNATDRKYLVIIGDL 109

RESULT 35  
US-09-999-831A-162  
; Sequence 162, Application US/09999831A  
; Publication No. US20040048332A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C68  
; CURRENT APPLICATION NUMBER: US/09/999,831A  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 162  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-999-831A-162

Query Match 42.1%; Score 296; DB 11; Length 224;

Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;  
  
QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVVSFLFVSGIVNFGYLSASEGEQFCI 60  
Db 1 MEGGAYGAGKAGGAFDLRRFLTPQVVARAVCLVFLVFSCLYGGYNAHESKQMYCV 60  
  
QY 61 YNRPNACSYGVAVGLAFITLCLLYALDVPFQISSVKDKKAVLSDI 109  
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDVDFYFQISNATDRKYLVIIGDL 109

RESULT 36  
US-09-978-824-162  
; Sequence 162, Application US/09978824  
; Publication No. US20050124789A9  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C14  
; CURRENT APPLICATION NUMBER: US/09/978,824  
; CURRENT FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20

1 PRIOR APPLICATION NUMBER: 60/078936  
2 PRIOR FILING DATE: 1998-03-20  
3 PRIOR APPLICATION NUMBER: 60/078910  
4 PRIOR FILING DATE: 1998-03-20  
5 PRIOR APPLICATION NUMBER: 60/078939  
6 PRIOR FILING DATE: 1998-03-20  
7 PRIOR APPLICATION NUMBER: 60/079294  
8 PRIOR FILING DATE: 1998-03-25  
9 PRIOR APPLICATION NUMBER: 60/079656  
10 PRIOR FILING DATE: 1998-03-26  
11 PRIOR APPLICATION NUMBER: 60/079664  
12 PRIOR FILING DATE: 1998-03-27  
13 PRIOR APPLICATION NUMBER: 60/079689  
14 PRIOR FILING DATE: 1998-03-27  
15 PRIOR APPLICATION NUMBER: 60/079663  
16 PRIOR FILING DATE: 1998-03-27  
17 PRIOR APPLICATION NUMBER: 60/079728  
18 PRIOR FILING DATE: 1998-03-27  
19 PRIOR APPLICATION NUMBER: 60/079786  
20 PRIOR FILING DATE: 1998-03-27  
21 PRIOR APPLICATION NUMBER: 60/079920  
22 PRIOR FILING DATE: 1998-03-30  
23 PRIOR APPLICATION NUMBER: 60/079923  
24 PRIOR FILING DATE: 1998-03-30  
25 PRIOR APPLICATION NUMBER: 60/080105  
26 PRIOR FILING DATE: 1998-03-31  
27 PRIOR APPLICATION NUMBER: 60/080107  
28 PRIOR FILING DATE: 1998-03-31  
29 PRIOR APPLICATION NUMBER: 60/080165  
30 PRIOR FILING DATE: 1998-03-31  
31 PRIOR APPLICATION NUMBER: 60/080194  
32 PRIOR FILING DATE: 1998-03-31  
33 PRIOR APPLICATION NUMBER: 60/080327  
34 PRIOR FILING DATE: 1998-04-01  
35 PRIOR APPLICATION NUMBER: 60/080328  
36 PRIOR FILING DATE: 1998-04-01  
37 PRIOR APPLICATION NUMBER: 60/080333  
38 PRIOR FILING DATE: 1998-04-01  
39 PRIOR APPLICATION NUMBER: 60/080334  
40 PRIOR FILING DATE: 1998-04-01  
41 PRIOR APPLICATION NUMBER: 60/081070  
42 PRIOR FILING DATE: 1998-04-08  
43 PRIOR APPLICATION NUMBER: 60/081049  
44 PRIOR FILING DATE: 1998-04-08  
45 PRIOR APPLICATION NUMBER: 60/081071  
46 PRIOR FILING DATE: 1998-04-08  
47 PRIOR APPLICATION NUMBER: 60/081195  
48 PRIOR FILING DATE: 1998-04-08  
49 PRIOR APPLICATION NUMBER: 60/081203  
50 PRIOR FILING DATE: 1998-04-09  
51 PRIOR APPLICATION NUMBER: 60/081229  
52 PRIOR FILING DATE: 1998-04-09  
53 PRIOR APPLICATION NUMBER: 60/081955  
54 PRIOR FILING DATE: 1998-04-15  
55 PRIOR APPLICATION NUMBER: 60/081817  
56 PRIOR FILING DATE: 1998-04-15  
57 PRIOR APPLICATION NUMBER: 60/081819  
58 PRIOR FILING DATE: 1998-04-15  
59 PRIOR APPLICATION NUMBER: 60/081952  
60 PRIOR FILING DATE: 1998-04-15  
61 PRIOR APPLICATION NUMBER: 60/081838  
62 PRIOR FILING DATE: 1998-04-15  
63 PRIOR APPLICATION NUMBER: 60/082568  
64 PRIOR FILING DATE: 1998-04-21  
65 PRIOR APPLICATION NUMBER: 60/082569  
66 PRIOR FILING DATE: 1998-04-21  
67 PRIOR APPLICATION NUMBER: 60/082704  
68 PRIOR FILING DATE: 1998-04-22  
69 PRIOR APPLICATION NUMBER: 60/082804  
70 PRIOR FILING DATE: 1998-04-22  
71 PRIOR APPLICATION NUMBER: 60/082700  
72 PRIOR FILING DATE: 1998-04-22  
73 PRIOR APPLICATION NUMBER: 60/082797

74 PRIOR FILING DATE: 1998-04-22  
75 PRIOR APPLICATION NUMBER: 60/082796  
76 PRIOR FILING DATE: 1998-04-23  
77 PRIOR APPLICATION NUMBER: 60/083336  
78 PRIOR FILING DATE: 1998-04-27  
79 PRIOR APPLICATION NUMBER: 60/083322  
80 PRIOR FILING DATE: 1998-04-28  
81 PRIOR APPLICATION NUMBER: 60/083392  
82 PRIOR FILING DATE: 1998-04-29  
83 PRIOR APPLICATION NUMBER: 60/083495  
84 PRIOR FILING DATE: 1998-04-29  
85 PRIOR APPLICATION NUMBER: 60/083496  
86 PRIOR FILING DATE: 1998-04-29  
87 PRIOR APPLICATION NUMBER: 60/083499  
88 PRIOR FILING DATE: 1998-04-29  
89 PRIOR APPLICATION NUMBER: 60/083545  
90 PRIOR FILING DATE: 1998-04-29  
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92 PRIOR FILING DATE: 1998-04-29  
93 PRIOR APPLICATION NUMBER: 60/083558  
94 PRIOR FILING DATE: 1998-04-29  
95 PRIOR APPLICATION NUMBER: 60/083559  
96 PRIOR FILING DATE: 1998-04-29  
97 PRIOR APPLICATION NUMBER: 60/083500  
98 PRIOR FILING DATE: 1998-04-29  
99 PRIOR APPLICATION NUMBER: 60/083742  
100 PRIOR FILING DATE: 1998-04-30  
101 PRIOR APPLICATION NUMBER: 60/084366  
102 PRIOR FILING DATE: 1998-05-05  
103 PRIOR APPLICATION NUMBER: 60/084414  
104 PRIOR FILING DATE: 1998-05-06  
105 PRIOR APPLICATION NUMBER: 60/084441  
106 PRIOR FILING DATE: 1998-05-06  
107 PRIOR APPLICATION NUMBER: 60/084637  
108 PRIOR FILING DATE: 1998-05-07  
109 PRIOR APPLICATION NUMBER: 60/084639  
110 PRIOR FILING DATE: 1998-05-07  
111 PRIOR APPLICATION NUMBER: 60/084640  
112 PRIOR FILING DATE: 1998-05-07  
113 PRIOR APPLICATION NUMBER: 60/084598  
114 PRIOR FILING DATE: 1998-05-07  
115 PRIOR APPLICATION NUMBER: 60/084600  
116 PRIOR FILING DATE: 1998-5-07  
117 PRIOR APPLICATION NUMBER: 60/084627  
118 PRIOR FILING DATE: 1998-05-07  
119 PRIOR APPLICATION NUMBER: 60/084643  
120 PRIOR FILING DATE: 1998-05-07  
121 PRIOR APPLICATION NUMBER: 60/085339  
122 PRIOR FILING DATE: 1998-05-13  
123 PRIOR APPLICATION NUMBER: 60/085338  
124 PRIOR FILING DATE: 1998-05-13  
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127 PRIOR APPLICATION NUMBER: 60/085582  
128 PRIOR FILING DATE: 1998-05-15  
129 PRIOR APPLICATION NUMBER: 60/085700  
130 PRIOR FILING DATE: 1998-05-15  
131 PRIOR APPLICATION NUMBER: 60/085689  
132 PRIOR FILING DATE: 1998-05-15  
133 PRIOR APPLICATION NUMBER: 60/085579  
134 PRIOR FILING DATE: 1998-05-15  
135 PRIOR APPLICATION NUMBER: 60/085580  
136 PRIOR FILING DATE: 1998-05-15  
137 PRIOR APPLICATION NUMBER: 60/085573  
138 PRIOR FILING DATE: 1998-05-15  
139 PRIOR APPLICATION NUMBER: 60/085704  
140 PRIOR FILING DATE: 1998-05-15  
141 PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 12; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;



QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHHTILRVVSWLFSIVVFGSIVNEGYNLSASGEQFCI 60  
DB 1 MESGAYGAAGAGGSFLLRRFLTQPVVARAVCLVFLVFSICVYGEYSNAHESKQYCV 60  
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109  
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109

RESULT 37

US-10-017-081A-162  
; Sequence 162, Application US/10017081A  
; Publication No. US20030049684A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C69  
; CURRENT APPLICATION NUMBER: US/10/017,081A  
; CURRENT FILING DATE: 2002-04-30  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 624  
; SEQ ID NO 162  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-081A-162

Query Match 42.1%; Score 296; DB 14; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHHTILRVVSWLFSIVVFGSIVNEGYNLSASGEQFCI 60  
DB 1 MESGAYGAAGAGGSFLLRRFLTQPVVARAVCLVFLVFSICVYGEYSNAHESKQYCV 60  
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109  
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109

RESULT 38

US-10-167-749-162  
; Sequence 162, Application US/10167749  
; Publication No. US20030056137A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C60  
; CURRENT APPLICATION NUMBER: US/10/167,749  
; CURRENT FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 624  
; SEQ ID NO 162  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-167-749-162

Query Match 42.1%; Score 296; DB 14; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHHTILRVVSWLFSIVVFGSIVNEGYNLSASGEQFCI 60  
DB 1 MESGAYGAAGAGGSFLLRRFLTQPVVARAVCLVFLVFSICVYGEYSNAHESKQYCV 60  
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109  
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109

RESULT 39

US-10-013-921A-162  
; Sequence 162, Application US/10013921A  
; Publication No. US20030068648A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: F2630PIC84  
; CURRENT APPLICATION NUMBER: US/10/013,921A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
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; PRIOR APPLICATION NUMBER: 60/079656  
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; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MEGAYGAGKAGGAFDPVTLRQPHHTILRVVSLFISWFGSIWEGYLSASGEQFCI 60
Db 1 MEGAYGAGKAGGAFDPVTLRQPHHTILRVVSLFISWFGSIWEGYLSASGEQFCI 60
Qy 61 YNRNPNACSYGAVGVLAFLTLCLLYLALDVYFPQISSVKDKKAVLSDI 109
Db 61 FNRNEDACRYCSAIGVLAFSLASAFLLVVDYFPQISNATDKKYLVIIGDL 109

RESULT 40
US-10-013-929A-162
; Sequence 162, Application US/10013929A
; Publication No. US20030072745A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC89
; CURRENT APPLICATION NUMBER: US/10/013,929A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27



```

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC59
; CURRENT APPLICATION NUMBER: US/10/166,709A
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01

; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC59
; CURRENT APPLICATION NUMBER: US/10/166,709A
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC59
; CURRENT APPLICATION NUMBER: US/10/016,177A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 02/002-04-30
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-016-177A-162

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MEGAYGAGKAGGAFDPYTLVRQPHITLRVVSWLFSIVFSGIVNFGYLSASEGQFCI 60
Db 1 MEGAYGAAKAGSGFDRRLTQPVVARAVCLVFLALIVFCIYGGYSNAHESKQMYCV 60

Qy 61 YNRPNACSYGVAVGVLAFLITCLLYLALDYFFQISVKDKKXAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFSLASAFFLVVDAYFPQISNATDKRYLVIGDL 109

RESULT 42
US-10-166-709A-162
; Sequence 162, Application US/10166709A
; Publication No. US20030104536A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.

```



APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC39  
CURRENT APPLICATION NUMBER: US/10/143,031A  
CURRENT FILING DATE: 2002-10-10  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/918585  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/07450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/077791  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 162  
LENGTH: 224  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-143-031A-162

Query Match 42.1%; Score 296; DB 14; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MEGGAYGAGKAGGAFDPTLVROPHTILRVVWLFSLVFGSIIVNGYLSASGEQFCI 60  
Db 1 MESSGAYGAAGAGGFDLRRFLTPQVVVARAVCLVFLVFSCTYVGGYSNAHESKQMYCV 60

Qy 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFQISSVKDKKAVLSDI 109  
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFFQISNATDKKYLIVIGDL 109

RESULT 44  
US-10-143-030A-162  
Sequence 162, Application US/10143030A  
Publication No. US20030147901A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC33  
CURRENT APPLICATION NUMBER: US/10/143,030A  
CURRENT FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: 60/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/07450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 162  
LENGTH: 224  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-143-030A-162

Query Match 42.1%; Score 296; DB 14; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MEGGAYGAGKAGGAFDPTLVROPHTILRVVWLFSLVFGSIIVNGYLSASGEQFCI 60  
Db 1 MESSGAYGAAGAGGFDLRRFLTPQVVVARAVCLVFLVFSCTYVGGYSNAHESKQMYCV 60

Qy 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFQISSVKDKKAVLSDI 109  
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFFQISNATDKKYLIVIGDL 109

RESULT 45  
US-10-002-967A-162  
Sequence 162, Application US/10002967A  
Publication No. US20030148373A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630PIC72  
 ; CURRENT APPLICATION NUMBER: US/10/002,967A  
 ; CURRENT FILING DATE: 2001-10-24  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/064249  
 ; PRIOR FILING DATE: 1997-11-03  
 ; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066364  
 ; PRIOR FILING DATE: 1997-11-21  
 ; PRIOR APPLICATION NUMBER: 60/077450  
 ; PRIOR FILING DATE: 1998-03-10  
 ; PRIOR APPLICATION NUMBER: 60/077632  
 ; PRIOR FILING DATE: 1998-03-11  
 ; PRIOR APPLICATION NUMBER: 60/077641  
 ; PRIOR FILING DATE: 1998-03-11  
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 ; PRIOR FILING DATE: 1998-03-11  
 ; PRIOR APPLICATION NUMBER: 60/077791  
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 ; PRIOR FILING DATE: 1998-03-13  
 ; PRIOR APPLICATION NUMBER: 60/078886  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/078936  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/078939  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
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 ; PRIOR APPLICATION NUMBER: 60/079664  
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 ; PRIOR APPLICATION NUMBER: 60/079689  
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 ; PRIOR APPLICATION NUMBER: 60/079920  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 60/079923  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 60/080105  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080107  
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 ; PRIOR FILING DATE: 1998-03-31  
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 ; PRIOR APPLICATION NUMBER: 60/080327  
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 ; PRIOR FILING DATE: 1998-04-01  
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 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080334  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/081070  
 ; PRIOR FILING DATE: 1998-04-08  
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 ; PRIOR APPLICATION NUMBER: 60/081071  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081195  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081203  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081229  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081955  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081817  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081819  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081952  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081838  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/082568  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/082569  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/082704  
 ; PRIOR FILING DATE: 1998-04-22  
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 ; PRIOR APPLICATION NUMBER: 60/082700  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082797  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082796  
 ; PRIOR FILING DATE: 1998-04-23  
 ; PRIOR APPLICATION NUMBER: 60/083336  
 ; PRIOR FILING DATE: 1998-04-27  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/083392  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083495  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083496  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083499  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083545  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083554  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083558  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083559  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083500  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083742  
 ; PRIOR FILING DATE: 1998-04-30



RESULT 46  
US-10-017-083A-152  
; Sequence 162, Application US/10017083A  
; Publication No. US20030148376A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Flvvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Garber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

RESULT 47

US-10-145-128A-162

; Sequence 162, Application US/10145128A

; Publication No. US20030157615A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Flvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Garber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoli, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmitted

```

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC46
; CURRENT APPLICATION NUMBER: US/10/145,128A
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-128A-162

```

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Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

```

```

QY 1 MEGGAGKAGKAGGAPYTLVRPHITLWVLSFIVVFGSTVNGVYLSASGEQFCI 60
Db 1 MESGAYGAKAGGSFDRFLTPQVVARAVCLVFLVFCIYGGYNAHESKOMYCV 60
QY 61 YNRPNACSYGAVGVLAFLITCLLYLALDVYFPQISSVKDRKXAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109

```

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RESULT 48
US-10-017-191A-162
; Sequence 162, Application US/10017191A
; Publication No. US20030170254A1
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

```

```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC62
; CURRENT APPLICATION NUMBER: US/10/017,191A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01

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; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
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; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
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; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-21  
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; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
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; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
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; PRIOR APPLICATION NUMBER: 60/083500  
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; PRIOR APPLICATION NUMBER: 60/083742  
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; PRIOR APPLICATION NUMBER: 60/084366  
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; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598

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; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
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Query Match 42.1%; Score 296; DB 14; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;  
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QY 1 MEGGAGACKAGGADPYTLVRQPHILRVSWLFSIVVFGSTVNEGYLNSASEGQFCI 60  
DB 1 MESGAYGAAGAGSGFDRRLFTQPVVARAVCLVFLVFCIYGGYNAHESKQMYCV 60  
;  
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVPFPQISSVKDRKAVLSDI 109  
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109  
;  
RESULT 49  
US-10-143-028A-162  
; Sequence 162, Application US/10143028A  
; Publication No. US20030180310A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey



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2	PRIOR FILING DATE: 1998-04-01
3	PRIOR APPLICATION NUMBER: 60/081070
4	PRIOR FILING DATE: 1998-04-08
5	PRIOR APPLICATION NUMBER: 60/081049
6	PRIOR FILING DATE: 1998-04-08
7	PRIOR APPLICATION NUMBER: 60/081071
8	PRIOR FILING DATE: 1998-04-08
9	PRIOR APPLICATION NUMBER: 60/081195
10	PRIOR FILING DATE: 1998-04-08
11	PRIOR APPLICATION NUMBER: 60/081203
12	PRIOR FILING DATE: 1998-04-09
13	PRIOR APPLICATION NUMBER: 60/081229
14	PRIOR FILING DATE: 1998-04-09
15	PRIOR APPLICATION NUMBER: 60/081955
16	PRIOR FILING DATE: 1998-04-15
17	PRIOR APPLICATION NUMBER: 60/081817
18	PRIOR FILING DATE: 1998-04-15
19	PRIOR APPLICATION NUMBER: 60/081819
20	PRIOR FILING DATE: 1998-04-15
21	PRIOR APPLICATION NUMBER: 60/081952
22	PRIOR FILING DATE: 1998-04-15
23	PRIOR APPLICATION NUMBER: 60/081838
24	PRIOR FILING DATE: 1998-04-15
25	PRIOR APPLICATION NUMBER: 60/082568
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31	PRIOR APPLICATION NUMBER: 60/082804
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35	PRIOR APPLICATION NUMBER: 60/082797
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47	PRIOR APPLICATION NUMBER: 60/083496
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55	PRIOR APPLICATION NUMBER: 60/084366
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64	PRIOR FILING DATE: 1998-05-07
65	PRIOR APPLICATION NUMBER: 60/084640

1	PRIOR FILING DATE: 1998-05-07	
2	PRIOR APPLICATION NUMBER: 60/084598	
3	PRIOR FILING DATE: 1998-05-07	
4	PRIOR APPLICATION NUMBER: 60/084600	
5	PRIOR FILING DATE: 1998-05-07	
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8	PRIOR APPLICATION NUMBER: 60/084643	
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15	PRIOR FILING DATE: 1998-05-13	
16	PRIOR APPLICATION NUMBER: 60/085582	
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22	PRIOR APPLICATION NUMBER: 60/085579	
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24	PRIOR APPLICATION NUMBER: 60/085580	
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26	PRIOR APPLICATION NUMBER: 60/085573	
27	PRIOR FILING DATE: 1998-05-15	
28	PRIOR APPLICATION NUMBER: 60/085704	
29	PRIOR FILING DATE: 1998-05-15	
30	PRIOR APPLICATION NUMBER: 60/085697	

Query Match	42.1%;	Score 296;	DB 14;	Length 224;
Best Local Similarity	48.6%;	Pred. No. 1.2e-25;		
Matches	53;	Conservative	19;	Mismatches 37; Indels 0; Gaps 0;
Qy:	1	MEGGAYCAGKAGAFDPYTLVROPHITLTVVSMLEFSIWFVGSIVNEGYLSNASEGEOPCI	60	
Db	1	MESGAYGAAXAGGSFDLRRELTPOQVVAVARCVLFALVFSCIYGEYGVSNAHESKOMVCV	60	
Qy:	61	YNRNPACSGVAVGLAFLTCLLLYLALDVVFPOISSVKORKKVLSDI	109	
Db	61	FNRNEDACRYGSAIGVLFAFLASAFFLVVDAYFPQISNATRKXLYVGDL	109	

Search completed: August 11, 2005, 08:26:04  
Job time : 62 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 16 Seconds  
(without alignments)  
793.788 Million cell updates/sec

Title: US-10-643-836-297  
Perfect score: 703  
Sequence: 1 MEGGAYGAGKAGGAFDPTL.....GEPHPAGTCTESTRGCGPG 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	27.3	247	T43324	synaptogyrin homolog
2	156	22.2	223	F89567	protein T08A9.3 [i
3	80	11.4	468	F84131	PTS system, mann
4	78	11.1	392	A44167	aminomethyltransf
5	75.5	10.7	348	B70743	hypothetical prote
6	73.5	10.5	1047	T14897	probable ATPase (E
7	73	10.4	407	VCB8PH	coat protein precu
8	73	10.4	455	1 OOOCCG	rhodopsin - giant
9	72	10.2	242	A49489	trypsin (EC 3.4.21
10	72	10.2	688	A53330	collagen alpha 2(I
11	71.5	10.2	311	T44610	cytochrome a3 con
12	71.5	10.2	344	T45774	odorant receptor 1
13	71.5	10.2	400	A41679	beta-3-adrenergic
14	71	10.1	114	A71905	hypothetical prote
15	71	10.1	386	A87697	Degr/DmrJ/EryC1/St
16	71	10.1	402	T39792	multidrug-efflux t
17	71	10.1	441	A48959	glutamate-1-semial
18	71	10.1	706	1 QBBE6L	glycoprotein H - h
19	70.5	10.0	202	A81008	hemolysin, probabl
20	70.5	10.0	226	2 C89982	hypothetical prote
21	70.5	10.0	317	T19143	hypothetical prote
22	70.5	10.0	471	T37887	hypothetical prote
23	70.5	10.0	663	F90291	large surface anti
24	70	10.0	365	1 SAVLNE	nitric oxide reduc
25	70	10.0	448	2 AH0395	nitric oxide reduc
26	70	10.0	448	2 B98191	PTS system, mann
27	70	10.0	512	2 H90010	voltage-dependent
28	70	10.0	1610	2 A46227	
29	70	10.0	1646	2 JH0422	

30	70	10.0	2161	2 JH0564	calcium channel al
31	70	10.0	2181	2 A38198	voltage-dependent
32	70	10.0	2203	2 T42742	beta 3-adrenergic
33	69.5	9.9	400	2 A53281	alpha 2-adrenocept
34	69.5	9.9	432	2 I50829	cellulose synthase
35	69.5	9.9	809	2 S16266	probable membrane
36	69.5	9.9	873	2 S46584	glutamate synthase
37	69.5	9.9	1530	2 E82085	halorhodopsin - Ha
38	69	9.8	239	2 A56808	putrescine-ornithi
39	69	9.8	427	2 F97790	probable cytochrom
40	69	9.8	537	2 T02450	hypothetical prote
41	68.5	9.7	163	2 B84731	matrix protein M2
42	68.5	9.7	195	1 MFIV2C	matrix protein M2
43	68.5	9.7	195	1 MFIV2W	matrix protein M2
44	68.5	9.7	195	1 MFIVB2	cation-transportin
45	68.5	9.7	902	2 C83964	collagen alpha 2(I
46	68.5	9.7	964	1 CGCH2S	phosphatidylglycer
47	68	9.7	201	2 B71635	probable isopropyl
48	68	9.7	362	2 T38621	phosphotransferase
49	68	9.7	518	1 S22385	collagen alpha 2(I
50	68	9.7	618	2 S32436	

ALIGNMENTS

RESULT 1

T43324  
synaptogyrin homolog - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43324  
R;Nonet, M.  
submitted to the EMBL Data Library, July 1998  
A;Description: Visualization of presynaptic terminal specializations in live C. elegans  
A;Reference number: Z22427  
A;Accession: T43324  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-247 <NON>  
A;Cross-references: UNIPROT:O76735; EMBL:AF079373; PIDN:AAC27798.1  
C;Genetics:  
C;Superfamily: Caenorhabditis elegans synaptogyrin homolog

Query Match 27.3%; Score 192; DB 2; Length 247;  
Best Local Similarity 36.1%; Pred.No. 5.8e-12;  
Matches 39; Conservative 22; Mismatches 47; Indels 0; Gaps 0;

QY 5 AYGAGKAGGAFDPTLVRQPHITLVRVSWLFSIVFSGIVNEGYLNSASGEQFCIYNRN 64

DB 6 AYGAGLAGANFDKNTFFKPTVLFRCALLFGLILWVSVSKGWHKPSDAIHPVCLYGRS 65

QY 65 PNACSYGVAVGVLAFTLLLYLALDVYFPOISSVKDRKKAVLSDIGVS 112

DB 66 SSTCSPATAVGFFAVCGAIVLIVLDARMDQISSVPTRRRAVLADLVVS 113

RESULT 2

F89567  
protein T08A9.3 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Nov-2001  
C;Accession: F89567  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: F89567  
A;Status: preliminary  
A;Molecule type: DNA





T14897  
probable ATPase (EC 3.6.1.-) - Leishmania donovani  
C:Species: Leishmania donovani  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T14897  
R:Meade, J.C.; Xue, L.; Case, S.T.  
A:Description: Leishmania donovani contains a family of p-type ion motive ATPase genes.  
A:Reference number: Z18256  
A:Accession: T14897  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1047 <MEA>  
A:Cross-references: UNIPROT:O61136; EMBL:AF067495; NID:g3192903; PIDN:AA01  
C:Genetics:  
A:Gene: CAL  
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C:Keywords: hydrolase; ion transport  
F:577-751/Domain: ATPase nucleotide-binding domain homology <ATN>  
  
Query Match 10.4%; Score 73.5; DB 2; Length 1047;  
Best Local Similarity 30.3%; Pred. No. 29;  
Matches 30; Conservative 16; Mismatches 38; Indels 15; Gaps 6;  
  
QY 5 AYAGKAGGAFDPTLVROPHTILRVSWLFSIVFGSIVNEG-----YLSASEGSEQ 57  
DB 871 AFGLYFGLLIHSYT-VRHPRVISFPRMMLDNKWFSGVLGGALFVPVIYINAIAGH-- 927  
  
QY 58 FCIYNNRNACSGV-AVGVLAPLT-CLLYLAL-DVFFP 93  
DB 928 --LFVHSMITWGVAVGVTFLAICETYKVIKNLFF 964  
  
RESULT 7  
VCBBFH  
N:Contains: coat protein precursor - flock house virus  
N:Contains: coat protein alpha; coat protein beta; coat protein gamma  
C:Species: flock house virus  
C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: B34011; S11037  
R:Dasgupta, R.; Sgro, J.Y.  
Nucleic Acids Res. 17, 7525-7526, 1989  
A:Title: Nucleotide sequences of three nodavirus RNA2's: the messenger for their coat pr  
A:Reference number: A34011; MUID:90016821; PMID:2798110  
A:Accession: B34011  
A:Molecule type: genomic RNA  
A:Residues: 1-407 <DAS>  
A:Cross-references: UNIPROT:P12870; EMBL:X15959; NID:g59265; PIDN:CAA34081.1; PID:g59266  
R:Kaesberg, P.; Dasgupta, R.; Sgro, J.Y.; Wery, J.P.; Selling, B.H.; Hosur, M.V.; Johnsd  
J. Mol. Biol. 214, 423-435, 1990  
A:Title: Structural homology among four nodaviruses as deduced by sequencing and X-ray c  
A:Reference number: S11036; MUID:90339486; PMID:2116525  
A:Contents: annotation  
C:Genetics:  
A:Map position: segment 2  
C:Superfamily: black beetle virus coat protein  
C:Keywords: coat protein; RNA binding  
F:1-407/Product: coat protein alpha #status predicted <ALP>  
F:1-363/Product: coat protein beta #status predicted <BET>  
F:35-49/Region: arginine-rich RNA-binding pattern  
F:364-407/Product: coat protein gamma #status predicted <GAM>  
F:363-364/cleavage site: Asn-Ala (autolytic) #status predicted  
  
Query Match 10.4%; Score 73; DB 1; Length 407;  
Best Local Similarity 28.9%; Pred. No. 12;  
Matches 35; Conservative 15; Mismatches 57; Indels 14; Gaps 5;  
  
QY 12 GGAFDPTLVROPHTILRVSW--LFSIVFGSIVNGSIVNEGQFCI-YNRNPNAC 68  
DB 270 GSTGQPTMDSGAATSGVWGNGMNDITIVIRVS-APEGAVNSAILKAWSCIEVRPNAM 328  
QY 69 SYGVA-----YGVLAFLTCLLYLALDVVFPQISSVKDKRAVL--SDIGVSGEPHPA 118

DB 329 LYQFGHDSPLDEVALQEQYRTVARSPLVAVIAAQNASHWVRVKSIIKSSLAASNIPGPI 388  
QY 119 G 119  
DB 389 G 389  
  
RESULT 8  
OOOCG  
rhodopsin - giant octopus  
C:Species: Octopus dofleini (giant octopus)  
C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: S00610  
R:Ovchinnikov, Y.A.; Abdulaev, N.G.; Zolotarev, A.S.; Artamonov, I.D.; Beespalov, I.A.; De  
FEBS Lett. 232, 69-72, 1988  
A:Title: Octopus rhodopsin. Amino acid sequence deduced from cDNA.  
A:Reference number: S00610; MUID:88211878; PMID:3366250  
A:Accession: S00610  
A:Molecule type: mRNA  
A:Residues: 1-455 <OVC>  
A:Cross-references: UNIPROT:P09241; EMBL:X07797  
A:Note: the source is designated as Paroctopus defleini  
A:Note: part of this sequence was confirmed by protein sequencing  
C:Superfamily: octopus rhodopsin  
C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipop  
F:37-61/Domain: transmembrane #status predicted <TM1>  
F:74-98/Domain: transmembrane #status predicted <TM2>  
F:107-131/Domain: transmembrane #status predicted <TM3>  
F:153-177/Domain: transmembrane #status predicted <TM4>  
F:201-224/Domain: transmembrane #status predicted <TM5>  
F:263-286/Domain: transmembrane #status predicted <TM6>  
F:302-323/Domain: transmembrane #status predicted <TM7>  
F:9,15/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:306/Binding site: retinal (Lys) (covalent) #status predicted  
F:337,338/Binding site: palmitate (Cys) (covalent) #status predicted  
  
Query Match 10.4%; Score 73; DB 1; Length 455;  
Best Local Similarity 24.6%; Pred. No. 14;  
Matches 31; Conservative 21; Mismatches 38; Indels 36; Gaps 6;  
  
QY 9 GKAGGAF-----DPYTLVRQHTILRVVS-----MLFSIV-----V 39  
DB 113 GLLGGIFGMSINTWAMISIDRYNIGRPMASAKKSHRRAFILMIFVWMNSLIVWSVGPV 172  
QY 40 F--GSIVNEGYSASEGQFCIYNNRNACSGVAVGLAFILTLCLLYLALDVYFPQISS 97  
DB 173 FWGAVVPEGLITSCS----FDYLTDPSTRSFILCMYFCGFWLPIIIIAF-CYFNIVMS 227  
QY 98 VKDRKK 103  
DB 228 VSNHEK 233  
  
RESULT 9  
S49489  
trypsin (EC 3.4.21.4) precursor - Paranotothenia magellanica  
C:Species: Paranotothenia magellanica  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S49489  
R:Genicot, S.; Rentier-Delrue, F.; Edwards, D.; van Beeumen, J.; Dodson, G.; Gerday, C.  
Submitted to the EMBL Data Library, October 1994  
A:Description: Trypsin and trypsinogen from an antarctic fish: molecular basis of cold a  
A:Reference number: S49489  
A:Accession: S49489  
A:Molecule type: mRNA  
A:Residues: 1-242 <GEN>  
A:Cross-references: UNIPROT:Q92099; EMBL:X82223; NID:g59507; PIDN:CAA57701.1; PID:g5595  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:1-13/Domain: signal sequence #status predicted <SIG>  
F:14-242/Product: trypsin #status predicted <MAT>  
F:21-235/Domain: trypsin homology <TRY>

Query Match 10.2%; Score 72; DB 2; Length 242;  
 Best Local Similarity 25.0%; Pred. No. 8.8; Mismatches 16; Indels 52; Gaps 7;  
 Matches 36; Conservative 16; Mismatches 40; Indels 52; Gaps 7;

QY 12 GGAFDPTLVRQPHITLVRVSWLFSVWFGSIWEGYLSA-----52  
 Db 24 GKESFYS---QPHQVSLNSGYHF---CGSLVNWNVVSAACHYKSRVVEVMGEHHRV 77

QY 53 SEG-BOFCYTN---RNPNCAGVAVGVLAFLTCLLYLALDVFPPOISSVKDKKAVLSD 108  
 Db 78 TEGKEQFISSSRVIRHPNTYSSVINDIML-----IKLSKPATLQ 118

QY 109 -----ICVSGEPHPAGTCTESTEG 128  
 Db 119 YVQVALPSSCAPAGTCTVSGWG 142

RESULT 10  
 A53330  
 collagen alpha 2(IX) chain precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
 C:Accession: A53330; S22216  
 R:Peraelae, M.; Elima, K.; Metsaeranta, M.; Rosati, R.; de Crombrughe, B.; Vuorio, E.  
 J. Biol. Chem. 269, 5064-5071, 1994  
 A:Title: The exon structure of the mouse alpha2(IX) collagen gene shows unexpected diver  
 A:Reference number: A53330; MUID:94148964; PMID:8106484  
 A:Accession: A53330  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-688 <PER>  
 A:Cross-references: UNIPROT:Q07643; GB:222923; NID:g311949; PIDN:CAA80503.1; PID:g311950  
 R:Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Cro  
 Biochim. Biophys. Acta 1130, 78-80, 1992  
 A:Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN  
 A:Reference number: S22215; MUID:92182017; PMID:1543751  
 A:Accession: S22216  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 521-524, 'M', 526-609, 'R', 611-665, 'G', 667-668 <ELI>  
 A:Cross-references: EMBL:X63014; NID:g49810; PIDN:CAA44742.1; PID:g49811  
 A:Note: the authors translated the codon GAC for residue 526 as His and GGT for residue  
 C:Genetics: 24/3; 49/3; 61/3; 82/3; 100/3; 112/3; 120/3; 138/3; 156/3; 172/3; 191/3; 209/  
 3; 534/1; 597/1; 623/1  
 C:Keywords: coiled coil; extracellular matrix; glycoprotein; heterotrimer; hydroxyllysine

Query Match 10.2%; Score 72; DB 2; Length 688;  
 Best Local Similarity 42.4%; Pred. No. 27; Mismatches 16; Indels 0; Gaps 0;  
 Matches 14; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 100 DRKAVLSDIGVSGEPHPAGTCTESTEGCPG 132  
 Db 76 DGKPGIDGLMGAKGEPGVGTGKQGLPGP 108

RESULT 11  
 T44610  
 cytochrome aa3 controlling protein [imported] - Bacillus cereus  
 C:Species: Bacillus cereus  
 C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
 C:Accession: T44610  
 R:Okstad, O.A.; Hegna, I.; Lindbaeck, T.; Rishovd, A.L.; Kolsto, A.B.  
 Microbiology 145, 621-631, 1999  
 A:Title: Genome organisation is not conserved between Bacillus cereus and Bacillus subtil  
 A:Reference number: Z22811; MUID:99231848; PMID:10217496  
 A:Accession: T44610  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-311 <OKS>  
 A:Cross-references: UNIPROT:Q9XBJO; EMBL:AJ010111; NID:g4584147; PIDN:CAB40605.1; PID:g4  
 A:Experimental source: ATCC 10987  
 C:Genetics:

A:Note: ctaa  
 C:Superfamily: cytochrome caa3 oxidase ctaa

Query Match 10.2%; Score 71.5; DB 2; Length 311;  
 Best Local Similarity 20.7%; Pred. No. 13; Mismatches 28; Conservative 27; Mismatches 39; Indels 41; Gaps 7;

QY 3 GGAYGAGKA---CGAFDP-----YTLVRQPH-----TILRVVSWLFF-----35  
 Db 30 GSGQCGKSWPLCNGEFVPSNLSMETIIELSHRLTSGSAGILVTLCLLSWKYKXHVRET 89

QY 36 ---SIWFGSIWEGYLSASGEQFCIYNNRPNACSYGVAVGVLAFL-----LTCLLYLA 87  
 Db 90 KTLAILSFVFLVAQALMGAAA-----VVGQNPVLAITHFGISLISFASVILLTCLIF-E 143

QY 88 LDVYFPQISSVKDRK 102  
 Db 144 IDQKFDARSLIMDK 158

RESULT 12  
 I45774  
 odorant receptor 1 - channel catfish  
 C:Species: Ictalurus punctatus (channel catfish)  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: I45774  
 R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.  
 Cell 72, 657-666, 1993  
 A:Title: The family of genes encoding odorant receptors in the channel catfish.  
 A:Reference number: A45774; MUID:93201590; PMID:7916654  
 A:Accession: I45774  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <NGA>  
 A:Cross-references: UNIPROT:Q9PSU1  
 A:Experimental source: olfactory epithelium  
 A:Note: sequence extracted from NCBI backbone (NCBIP:127744)  
 C:Superfamily: olfactory receptor ORL4  
 C:Keywords: olfaction; transmembrane protein

Query Match 10.2%; Score 71.5; DB 2; Length 344;  
 Best Local Similarity 21.4%; Pred. No. 14; Mismatches 22; Conservative 21; Mismatches 43; Indels 17; Gaps 3;

QY 20 LVQRPHITLVRVSWLFSVWFGSIWEGYLSASGEQFC-----IYNNRPNACS 69  
 Db 143 VTKEAMTLIIIVITWIFSIIALLVALITRLSFCRSVIINSYFCDHGPTILLAGNDKFIN 202

QY 70 YGVAVGVLAFLTC-----LLYALDVYFPPOISSVKDRKAV 105  
 Db 203 RVNAGCFVLDQVFPLLIIVSYICIGIALMNISHGLERRKAM 245

RESULT 13  
 A41679  
 beta-3-adrenergic receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C:Accession: A41679  
 R:Muzzin, P.; Revelli, J.P.; Kuhne, F.; Gocayne, J.D.; McCombie, W.R.; Venter, J.C.; Giac  
 J. Biol. Chem. 266, 24053-24058, 1991  
 A:Title: An adipose tissue-specific beta-adrenergic receptor. Molecular cloning and down-  
 A:Reference number: A41679; MUID:92084710; PMID:1721063  
 A:Accession: A41679  
 A:Molecule type: mRNA  
 A:Residues: 1-400 <MUZ>  
 A:Cross-references: UNIPROT:P26255; GB:M74716; NID:g950087; PIDN:AAA74470.1; PID:g202766  
 A:Experimental source: brown adipose tissue  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
 F;8/6/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 71.5; DB 2; Length 400;

Best Local Similarity 26.0%; Pred. No. 17;  
Matches 39; Conservative 19; Mismatches 51; Indels 41; Gaps 9;

QY 14 APPYTLVQPHILR-----VSWLFSIVV-FGSIYNEGVLNSASGEQF 58  
DB 129 AVDRYLAVTNP-----LRYGLTVTKRARAVALVIVSATVSFAPIMSQWRVGADEAQB 185

QY 59 CIYRNPNACS-----YGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIG-- 110  
DB 186 C--HSNPRCCSPASNMPYALLSSVSFYLPLVW-LFVYARVFAKQRFRVRELGRF 242

QY 111 -----VSGEPHPA--GTPCTESTEGCP 130  
DB 243 PPESPRSPSRSPSPATVGTGP--TASDGV 270

RESULT 14  
A71905  
hypothetical protein jhp0647 - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: A71905  
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999  
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori  
A:Reference number: A71905; MUID:99120557; PMID:9923682  
A:Accession: A71905  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <ARN>  
A:Cross-references: UNIPROT:Q9ZLD3; GB:AE001497; GB:AE001439; NID:G4155199; PIDN:AA0623  
A:Experimental source: strain J99  
C:Genetics:  
A:Superfamily: Helicobacter pylori hypothetical protein HP0708

Query Match 10.1%; Score 71; DB 2; Length 114;  
Best Local Similarity 27.2%; Pred. No. 5;  
Matches 22; Conservative 20; Mismatches 17; Indels 22; Gaps 4;

QY 50 NSASEGQFC-----IYNRNPNACSYGVAVGVL----AFLTCL----LYLALD 89  
DB 6 HSNKERFVRIEDEKKELFAETNENPHGLSMALIGLVFGAFIALLVPKIYLSNN 65

QY 90 VYF--POISSYKRRKAVLS 108  
DB 66 IYVISRKINTLEDQKRLLEE 86

RESULT 15  
A87697  
DegN/DnrJ/BryC1/Strs family protein [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: A87697  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolonitskiy, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87697; MUID:21173698; PMID:11259647  
A:Accession: A87697  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-386 <STO>  
A:Cross-references: UNIPROT:Q9A2F4; GB:AE005673; NID:gl3425359; PIDN:AAK25573.1; GSPDB:C  
C:Genetics:  
A:Gene: CC3611  
C:Superfamily: erythromycin resistance protein

Query Match 10.1%; Score 71; DB 2; Length 386;

Best Local Similarity 26.4%; Pred. No. 18;  
Matches 28; Conservative 18; Mismatches 34; Indels 26; Gaps 6;

QY 5 AYGAGKAGGAPP-YTLVRQPHITLRLVSWLFSIVVFGSIYNEGVLNSASGEQFCIYNR 63  
DB 70 ANGIKGDVAFCPSTFAATP-----EVFPVADATPFVDVLPD-----TYNL 112

QY 64 NPNACSYGVAVGVLA--FLTCLLYLALDVY-----PQISSVKDRK 102  
DB 113 DPAKLEAALA-GVKABGQLTPKVIADVLFQGPADYPAIKAICDRE 157

RESULT 16  
I39792  
multidrug-efflux transporter blt - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39792; D6595  
R:Aghmed, M.; Lyass, L.; Markham, P.N.; Taylor, S.S.; Vazquez-Laslop, N.; Neyfakh, A.A. J. Bacteriol. 177, 3904-3910, 1995  
A:Title: Two highly similar multidrug transporters of Bacillus subtilis whose expression is induced by tetracycline  
A:Reference number: A57353; MUID:95332191; PMID:7608059  
A:Accession: I39792  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-400 <RES>  
A:Cross-references: UNIPROT:P39843; GB:I32599; NID:G483939; PIDN:AAC36944.1; PID:G483941  
R:Kunst, P.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, I.; Kech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hulio, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadai, V.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: D69595  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-400 <KUN>  
A:Cross-references: GB:Z99117; GB:AL009126; NID:G2634966; PIDN:CAB14600.1; PID:G2635104  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: blt  
C:Superfamily: tetracycline resistance protein  
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 10.1%; Score 71; DB 2; Length 400;  
Best Local Similarity 26.6%; Pred. No. 19;  
Matches 29; Conservative 20; Mismatches 40; Indels 20; Gaps 4;

QY 26 TILRVVSWLFSIVVFGSIYNEGVLNSASEG---OFCIYRNPNACSYGVAVGVLAFL- 80  
DB 258 TISSIVAVVIQVLLFGKLVNK-----LGEKRMICQLITGAILAFVSTVMSGFLTVLL 310

QY 81 -TCLLYLALDVYFPQISSVKDRKKAVLSDIGVSGEPHPAGTPCTESTEG 128  
DB 311 VTCTFIPLFDLLRLPT-----AHLNMGAGQGVAGNNSYTSISG 352

RESULT 17  
A48959  
Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Propionibacterium freudenreichii  
C:Species: Propionibacterium freudenreichii  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A48959

R;Murakami, K.; Hashimoto, Y.; Murooka, Y.  
Appl. Environ. Microbiol. 59, 347-350, 1993  
A;Title: Cloning and characterization of the gene encoding glutamate 1-semialdehyde 2,1-  
A;Reference number: A48959; MUID:93175878; PMID:8439165  
A;Accession: A48959  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-441 <MUR>  
A;Cross-references: UNIPROT:Q06774; GB:D85417; NID:G2347004; PIDN:BA21914.1; PID:G23470  
A;Note: sequence extracted from NCBI backbone (NCBIN:125567, NCBIP:125568)  
C;Superfamily: ornithine-oxo-acid aminotransferase  
C;Keywords: intramolecular transferase; isomerase

Query Match 10.1%; Score 71; DB 2; Length 441;  
Best Local Similarity 29.8%; Pred. No. 21;  
Matches 29; Conservative 11; Mismatches 34; Indels 26; Gaps 6;

QY 33 WLFISVVFSGSVNEG-----YLNASBGE--QFCIYNRNPNACSYGVAVGV 76  
DB 261 WTPDLTFGKVGGMPLAAGGSAQLMDYL--APGPPYQAGTLSGNPAACAAGLA--T 316  
QY 77 LAFPLCLLYLALDVPYFPQISSVKDRKKAVALSDIGVSGEPH 116  
DB 317 LALMDAAAYSRLDATADRVSMAD---AALESAGV---PH 350

RESULT 18  
Q06B6L  
glycoprotein H - human herpesvirus 4 (strain B95-8)  
C;Species: human herpesvirus 4, Epstein-Barr virus  
C;Date: 03-Aug-1984 #sequence revision 25-Feb-1985 #text\_change 09-Jul-2004  
C;Accession: A93065; A36827; A03795; S33046  
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.  
Mol. Biol. Med. 1, 21-45, 1983  
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus  
A;Reference number: A93065; MUID:85035713; PMID:6092825  
A;Accession: A93065  
A;Molecule type: DNA  
A;Residues: 1-116 <BAN>  
A;Cross-references: UNIPROT:P03231; EMBL:V01555  
R;Farrell, P.J.; Barrell, B.G.  
Submitted to the EMBL Data Library, June 1984  
A;Description: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
A;Reference number: A38059  
A;Accession: A36827  
A;Molecule type: DNA  
A;Residues: 1-706 <FAR>  
A;Cross-references: EMBL:V01555; NID:G59074; PIDN:CAA24797.1; PID:G1334905  
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H  
Nature 310, 207-211, 1984  
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
A;Reference number: A03794; MUID:84270667; PMID:6087149  
A;Contents: annotation; protein coding region  
A;Note: neither amino acid nor nucleotide sequence is given  
C;Superfamily: herpesvirus glycoprotein H  
C;Keywords: glycoprotein; transmembrane protein  
F;60,435,549,604,664/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 71; DB 1; Length 706;  
Best Local Similarity 26.4%; Pred. No. 35;  
Matches 34; Conservative 23; Mismatches 48; Indels 24; Gaps 7;

QY 2 EGGAYGAGKAGG-----AFDPYTLVRQPHTILRVVSMWLFISVVFSGSVNEGILNSASE 54  
DB 385 KAGVY-SGLIGGATSVLLSAYNRHPLFQPLHTVRETFLTGSHV-----LRELRLNVTTQ 439  
QY 55 GEQFCIYNRNPN-AS-----YGVAVGVLA--FLTCLLYLALDVPYFPQISSVKDRKK 103  
DB 440 GPNLALYQLLSTALCSALEITGEVLRGLGALGTESGLFSPCYLSRFLDTRDKLSMAP-QE 498  
QY 104 AVLSDIGVS 112  
DB 499 ATLDQAVS 507

RESULT 19  
A81008  
hemolysin, probable NMB2091 [imported] - Neisseria meningitidis (strain MC58 serogroup B).  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: A81008  
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755; PMID:10710307  
A;Accession: A81008  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-202 <TET>  
A;Cross-references: UNIPROT:Q9JXE1; GB:AE002558; GB:AE002098; NID:G7227345; PIDN:AAF42402  
A;Experimental source: serogroup B, strain MC58  
C;Genetics:  
A;Gene: NMB2091  
C;Superfamily: Probable periplasmic protein

Query Match 10.0%; Score 70.5; DB 2; Length 202;  
Best Local Similarity 24.5%; Pred. No. 10;  
Matches 25; Conservative 20; Mismatches 50; Indels 7; Gaps 3;

QY 23 QPHTILRVVSMWLFISVVFSGSVNEGILNSASEGEQFCIYNRNPNACSYGVAVGVLAFLFC 82  
DB 4 KPHTVRLIAAIFSLALSCV--SAVIGSAAVGAKSVDVRRTTGAQTDNVMALRIETTA 61  
QY 83 LLYLALD----VYFPQISSV-KDRKKAVALSDIGVSGEPHPAG 119  
DB 62 RSYLRQNNQTKYTPQISVGVGNRHLLLGQVATEGEKQFVG 103

RESULT 20  
C89982  
hypothetical protein [imported] - Staphylococcus aureus (strain N315)  
C;Species: Staphylococcus aureus  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: C89982  
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ul, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A;Reference number: A89758; MUID:21311952; PMID:11418146  
A;Accession: C89982  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-226 <KUR>  
A;Cross-references: UNIPROT:Q99SV6; GB:BA000018; PID:G13701725; PIDN:BA843018.1; GSPDB:G  
A;Experimental source: strain N315  
C;Genetics:  
A;Gene: SA1746

Query Match 10.0%; Score 70.5; DB 2; Length 226;  
Best Local Similarity 27.8%; Pred. No. 12;  
Matches 27; Conservative 20; Mismatches 27; Indels 23; Gaps 5;

QY 14 AFDPYTLVRQ---PH-----TILRVVSMWLFISVVFSGSVNEGILNSASEGEQFCIYNRP 65  
DB 139 ASQFQTELRVRKVPYGIYVFTIILVPFLFSIAIV--LVNYFVLSQSS-----FP 186  
QY 66 NACSIGVAVGVLAFLTCLLYLALDVPYFPQISSVKDRK 102  
DB 187 DLVSYTLNIG---FLIISIVILVNYFKQLNKINTRK 220

RESULT 21













F:586-606/Domain: transmembrane #status predicted <TM>

Query Match 9.9%; Score 69.5; DB 2; Length 809;  
Best Local Similarity 21.5%; Pred. No. 57;  
Matches 28; Conservative 24; Mismatches 51; Indels 27; Gaps 5;  
QY 4 GAYGAGKAGGAF---DPYTLV--RQPHITLTVSVWLFSSIVVFGSIVNVEGYLNSASEGQ 57  
Db 513 GICQSGAANAFHGLDPSIDFSRAHHAQMPN-----LAYMATVGFPTTYADLSQT 567  
QY 58 FCYNNRNPNACSGVAVGVLAFLTCLLYLALDVYFP-----QISSVKDRKKAVLS 107  
Db 568 AVVLPHPNAAATVG-----AYLDLMGFMAATWYVPVAGVDIVSADHVSVDVADRNLLVTS 621  
QY 108 DIGVSGEPHP 117  
Db 622 TLATSGEIAIP 631

RESULT 36  
S46584  
Probable membrane protein YJL094c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein J0909  
C;Species: Saccharomyces cerevisiae  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S46584; S56871; S47057  
R;Miosga, T.; Witzel, A.; Zimmermann, F.K.  
Yeast 10, 965-973, 1994  
A;Title: Sequence and function analysis of a 9.46 kb fragment of Saccharomyces cerevisiae  
A;Reference number: S46584; MUID:95076716; PMID:7985424  
A;Accession: S46584  
A;Molecule type: DNA  
A;Residues: 1-873 <MI>  
A;Cross-references: UNIPROT:P40309; EMBL:X77087; MID:g521093; PIDN:CA54359.1; PID:g521093  
A;Note: the authors translated the codon TCC for residue 645 as Trp  
R;Miosga, T.; Schaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chaltatzis, N.; Fourmies  
submitted to the Protein Sequence Database, September 1995  
A;Reference number: S56855  
A;Accession: S56871  
A;Molecule type: DNA  
A;Residues: 1-873 <MIW>  
A;Cross-references: EMBL:Z49369; MID:g1008267; PID:g1008268; MIPS:YJL094c  
C;Genetics:  
A;Gene: SGD:KHA1  
A;Cross-references: SGD:S0003630  
A;Map position: 10L  
C;Keywords: transmembrane protein

Query Match 9.9%; Score 69.5; DB 2; Length 873;  
Best Local Similarity 26.8%; Pred. No. 62;  
Matches 33; Conservative 17; Mismatches 46; Indels 27; Gaps 7;  
QY 17 PYTLVRQPHITLTVSVW-LFSIVVFGSIVNVEGYLNSASEGQFCIYNRNPNACSYGVAVG 75  
Db 43 PFSMWRQPKVISEVISGVILGPTFGQIPN--YNTTFPTSPGLNLVAN-----LG 93  
QY 76 VLAFITCLLYALDVYFPQISSVKDRKKAVLSDIGVSGEPHPAGTPC-----TES 125  
Db 94 IILF---MFLGLEVDIAFIK--KHLKKALV--IGIVTLAVPFGGCLLAIFLHTYANK 146  
QY 126 TEG 128  
Db 147 TEG 149

RESULT 37  
E82085  
Glutamate synthase (NADPH2) (EC 1.4.1.13) large chain [similarity] - Vibrio cholerae (serotype O1)

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: E82085  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1530 <HEI>  
A;Cross-references: UNIPROT:Q9KPU4; GB:AE004307; GB:AE003852; NID:g9656934; PIDN:AAF95516  
A;Experimental source: serogroup O1; strain Ni6961; biotype El Tor  
C;Genetics:  
A;Gene: VC2373  
A;Map position: 1  
C;Superfamily: Glutamate synthase, large subunit  
C;Keywords: 3Fe-4S; metalloprotein; oxidoreductase  
F;1-36/Domain: propeptide #status predicted <PRO>  
F;37-1530/Product: glutamate synthase #status predicted <MAT>  
F;37/Active site: Cys #status predicted  
F;1149,1155,1160/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 9.9%; Score 69.5; DB 2; Length 1530;  
Best Local Similarity 28.0%; Pred. No. 1.1e+02;  
Matches 26; Conservative 15; Mismatches 27; Indels 25; Gaps 6;  
QY 1 MEGGA---YCGAGKAGGAFDPYTLVRQPHITLTVSVW-LFSIVVFGSIVNVEGYLNSAS 53  
Db 1336 VEGDANDYWGKLSGG-----TLVLPNRNATVPEINIVWGVNVCYFGATSGESYIRGLA 1390  
QY 54 EGEQFCIYNR-----NPNACSY---GVAV 74  
Db 1391 -GERFCVRNAGKVVVEGIGDHGCEYMTGGVAV 1422

RESULT 38  
A56808  
halorhodopsin - Halobacteriaceae gen. sp. (fragment)  
C;Species: Halobacteriaceae gen. sp.  
C;Date: 25-Aug-1995 #sequence\_revision 25-Aug-1995 #text\_change 21-Jul-2000  
C;Accession: A56808; B56808  
R;Otsu, J.; Tomioka, H.; Saeabe, H.  
Biochim. Biophys. Acta 1112, 7-13, 1992  
A;Title: Properties and the primary structure of a new halorhodopsin from halobacterial  
A;Reference number: A56808; MUID:93041879; PMID:1420272  
A;Accession: A56808  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 25-239 <OTI>  
A;Experimental source: strain mex  
A;Note: sequence extracted from NCBI backbone (NCBI:118503, NCBIP:118504)

A;Accession: B56808  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-29 <OF>  
C;Superfamily: bacteriorhodopsin  
C;Keywords: photoreceptor; transmembrane protein

Query Match 9.8%; Score 69; DB 2; Length 239;  
Best Local Similarity 22.9%; Pred. No. 17;  
Matches 27; Conservative 17; Mismatches 42; Indels 32; Gaps 4;  
QY 7 GAGKAGGAFDPYTLVRQPHITLTVSVWLFSSIVVFGSIVNVEGYLNSASEGQFCIYNRNPN 66  
Db 89 GAGPEGGVTPWG-----RYLTWAFSTPMI--LIALGLLAGSNMSKLFATVAVDVG 137  
QY 67 ACSYGVAVGV-----LAFITCLLYALDVYFPQISSVKDRKKAVLSDI 109  
Db 138 MCITGLAALTTSSYLLRWVWVGISCAFFVWVYILLAEW-----AKDAEVAGTADI 189

RESULT 39  
F97790  
putrescine-ornithine antiporter [imported] - Rickettsia conorii (strain Malish 7)

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: F97790  
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001  
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A;Reference number: A97700; MUID:21442074; PMID:11557893  
C;Accession: F97790  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-427 <R>  
A;Cross-references: UNIPROT:Q92HP5; GB:AE006914; PIDN:AAL03264.1; PID:g15619819; GSPDB:G  
C;Genetics:  
A;Gene: potE  
C;Superfamily: L-lysine transport protein

Query Match 9.8%; Score 69; DB 2; Length 427;  
Best Local Similarity 26.8%; Pred. No. 32;  
Matches 22; Conservative 14; Mismatches 32; Indels 14; Gaps 2;

QY 33 WLFSLVFGSVNVEGLNS-----ASEG--EQFCIYNRNPACSYGVAVGLA 78  
Db 267 WSSVITVIAIICIGTLNWLVTSGQIALGLABDGLLPKFFAKKSNNAPTHGIIVCSLG 326  
QY 79 FLTCLLYLALDVVFPQISSVKD 100  
Db 327 IVPLLVFTANDNFAKQITQIID 348

RESULT 40  
T02450  
probable cytochrome P450 F4118.5 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: T02450; B84897  
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul matrix protein M2 - influenza B virus (strain B/Ann Arbor/1/66 [cold-adapted])  
A;Title: Sequence and analysis of the plant Arabidopsis thaliana.  
A;Reference number: Z14674  
A;Accession: T02450  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-537 <R>  
A;Cross-references: UNIPROT:O80823; EMBL:AC004665; NID:g3386593; PID:g3386598  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: B84897  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-537 <R>  
A;Cross-references: GB:AE002093; NID:g6598466; PIDN:AAC62873.2; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g45970; F4118.5  
A;Map position: 2  
C;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology  
F;302-480/Domain: cytochrome P450 homology <P45>

Query Match 9.8%; Score 69; DB 2; Length 537;  
Best Local Similarity 24.8%; Pred. No. 41;  
Matches 25; Conservative 17; Mismatches 47; Indels 12; Gaps 4;

QY 31 VSNLFSIVFGSVNVEGLNS-----ASEGEFCIYNRNPACSYGVAVGLAFITCLL 84  
Db 314 LSWFFWLITQHPAIEDKILREICTVLIVETRGDDVALVETDEPLSE---ELDRVLFLKAA 370

QY 85 YLALDVYFFQISSVKDKKAVLSDIGVSGEPHPAGTPTCTES 125  
Db 371 SETRLY-PSVP--EDSKRAVKDVLDPDGTFFVAGSSITVS 408

RESULT 41  
B84731  
hypothetical protein At2g32280 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B84731  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: B84731  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-163 <STO>  
A;Cross-references: UNIPROT:Q9ZV57; GB:AE002093; NID:g3831471; PIDN:AAC69953.1; GSPDB:GN  
C;Genetics:  
A;Gene: At2g32280  
A;Map position: 2

Query Match 9.7%; Score 68.5; DB 2; Length 163;  
Best Local Similarity 30.3%; Pred. No. 13;  
Matches 27; Conservative 12; Mismatches 41; Indels 9; Gaps 4;

QY 15 FDPYTLVRQPHITLIRVSVLFSIVVFGSVNVEGLNSASEGEQFCIYNRNPACSYGVAV 74  
Db 84 FORSSSTRQISMACLIVLTWIVFAVGFGSIVGTMSNKSRS--CGFTHH-HFLSTIG--- 137  
QY 75 GVLAFLTCLLYLALDVVFPQISSVKDRKK 103  
Db 138 GILCFEHALFCVA---YVSATAAKDEAK 163

RESULT 42  
MFTV2C  
matrix protein M2 - influenza B virus (strain B/Ann Arbor/1/66 [cold-adapted])  
C;Species: Influenza B virus  
C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C;Accession: B30064  
R;DeBorde, D.C.; Donabedian, A.M.; Herlocher, M.L.; Naeve, C.W.; Maassab, H.F. Virology 163, 429-443, 1988  
A;Title: Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66 influenza vi A;Reference number: A28604; MUID:88179548; PMID:3354202  
A;Accession: B30064  
A;Molecule type: genomic RNA  
A;Residues: 1-195 <DEB>  
A;Cross-references: UNIPROT:Pl3881  
C;Comment: The RNA sequence was obtained from GenBank, release 58.0.  
C;Genetics:  
A;Map position: segment 7  
C;Superfamily: influenza virus matrix protein M2  
C;Keywords: matrix protein

Query Match 9.7%; Score 68.5; DB 1; Length 195;  
Best Local Similarity 28.2%; Pred. No. 16;  
Matches 31; Conservative 15; Mismatches 47; Indels 17; Gaps 5;

QY 4 GAYGAGKAG--GAF---DPYTLVRQPHITLIRVSVLFSIVVFGSVNVEGLNSASEGEQF 58  
Db 65 GCNGSAKALYKGFSSCEIPIMLEPFQILSCPSILSALHF-MAWTIGHLNQIKRGVNL 123

QY 59 CIYNRNPACSYGVAVGLAFITCLLYLALDVYFFQISSVKDRKKAVLSD 108  
Db 124 KIRIRNPKNKTINREVSIILR-----HSYQKEIQ-A-KETMKEVLSLD 162

RESULT 43  
MFTV2W  
matrix protein M2 - influenza B virus (strain B/Ann Arbor/1/66 [wild-type])  
C;Species: influenza B virus  
C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004

C;Accession: D30064  
R;DeBorde, D.C.; Donabedian, A.M.; Herlocher, M.L.; Naevs, C.W.; Maaseab, H.F.  
Virology 163, 429-443, 1988  
A;Title: Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66 influenza virus  
A;Reference number: A28604; MUID:88179548; PMID:3354202  
A;Accession: D30064  
A;Molecule type: genomic RNA  
A;Residues: 1-195 <DEB>  
A;Cross-references: UNIPROT:P13882  
A;Comment: The RNA sequence was obtained from GenBank, release 58.0.  
C;Genetics:  
A;Map position: segment 7  
C;Superfamily: Influenza virus matrix protein M2  
C;Keywords: matrix protein

Query Match 9.7%; Score 68.5; DB 1; Length 195;  
Best Local Similarity 28.2%; Pred. No. 16;  
Matches 31; Conservative 15; Mismatches 47; Indels 17; Gaps 5;

QY 4 GAYGAGKAG--GAF---DPYTLVRQPHITLVRVSWLFSIVVFGSIVNMGYNSASGEQF 58  
DB 65 GCNGSAKAEYLGKFSCEETPIMLEPQILSICFSLALHF-MAWTIGHNLQIKRGVNL 123

QY 59 CIYNNRPNACSYGAVGVLAFLTCLLYLALDVYFPQISSVKRKAVALSD 108  
DB 124 KIRIRNPNKETINREVSILR-----HSYQKEIQK-KETMKEVLSD 162

RESULT 44  
MFIVB2  
matrix protein M2 - influenza B virus (strain B/Singapore/222/79)  
C;Species: influenza B virus  
C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: B25619  
R;Hiebert, S.W.; Williams, M.A.; Lamb, R.A.  
Virology 155, 747-751, 1986  
A;Title: Nucleotide sequence of RNA segment 7 of influenza B/Singapore/222/79: maintained  
A;Reference number: A94351; MUID:87071690; PMID:3788064  
A;Accession: B25619  
A;Molecule type: mRNA  
A;Residues: 1-195 <HIE>  
A;Cross-references: UNIPROT:P08383  
A;Note: the authors translated the codon CAT for residue 195 as Gln  
A;Comment: The RNA sequence was obtained from GenBank, release 52.0.  
C;Genetics:  
A;Map position: segment 7  
C;Superfamily: Influenza virus matrix protein M2  
C;Keywords: matrix protein

Query Match 9.7%; Score 68.5; DB 1; Length 195;  
Best Local Similarity 28.2%; Pred. No. 16;  
Matches 31; Conservative 15; Mismatches 47; Indels 17; Gaps 5;

QY 4 GAYGAGKAG--GAF---DPYTLVRQPHITLVRVSWLFSIVVFGSIVNMGYNSASGEQF 58  
DB 65 GCNGSAKAEYLGKFSCEETPIMLEPQILSICFSLALHF-MAWTIGHNLQIKRGVNL 123

QY 59 CIYNNRPNACSYGAVGVLAFLTCLLYLALDVYFPQISSVKRKAVALSD 108  
DB 124 KIRIRNPNKETINREVSILR-----HSYQKEIQK-KETMKEVLSD 162

RESULT 45  
C83964  
cation-transporting ATPase pacL [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: C83964  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: C83964

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-902 <STO>  
A;Cross-references: UNIPROT:Q9KX9; GB:BA000004; NID:g10174886; PIDN:BA062;  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: pacL  
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain 1

Query Match 9.7%; Score 68.5; DB 2; Length 902;  
Best Local Similarity 25.0%; Pred. No. 81;  
Matches 20; Conservative 17; Mismatches 34; Indels 9; Gaps 2;

QY 19 TLVRQPHITLVRVSWLFSIVVFGSIVNMGYNSASGEQFCIYNNRPNACSYGAVGVLA 78  
DB 798 TLQANPDDLTRAQSVAFVTLVMAQLIHVDFCRS-----EYSVFRHNPFFENKY----LVLA 848

QY 79 FLTCLLYLALDVYFPQISSV 98  
DB 849 VLSSVLLMLIVYPPLOQV 868

RESULT 46  
CGCH2S  
collagen alpha 2(I) chain precursor - chicken (fragments)  
C;Species: Gallus gallus (chicken)  
C;Date: 24-Apr-1984 #sequence\_revision 15-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: I50206; I50207; S07354; S10848; S10480; S11146; I50628; I50170; I50625; I50625;  
R;Boedtker, H.; Finer, M.; Aho, S.  
Ann. N. Y. Acad. Sci. 460, 85-116, 1985  
A;Title: The structure of the chicken alpha 2 collagen gene.  
A;Reference number: I50206; MUID:86185168; PMID:3868961  
A;Accession: I50206  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-245 <BOE>  
A;Cross-references: UNIPROT:P02467; GB:M25963; NID:g211581; PIDN:AAA69960.1; PID:g211605  
A;Accession: I50207  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 246-431 <BO2>  
A;Cross-references: GB:M25965; NID:g211583; PIDN:AAA69961.1; PID:g211606  
R;Aho, S.; Tate, V.; Boedtker, H.  
Nucleic Acids Res. 12, 6117-6125, 1984  
A;Title: Location of the 11 bp exon in the chicken pro alpha-2(I) collagen gene.  
A;Reference number: S07354; MUID:84297217; PMID:6473103  
A;Accession: S07354  
A;Molecule type: DNA  
A;Residues: 1-33 <AHO>  
A;Cross-references: EMBL:X00760; NID:g63266; PIDN:CAA25330.1; PID:g63267  
R;Tate, V.E.; Finer, M.H.; Boedtker, H.; Doty, P.  
Nucleic Acids Res. 11, 91-104, 1983  
A;Title: Chick pro-alpha-2 (I) collagen gene: exon location and coding potential for the  
A;Reference number: S10480; MUID:83246518; PMID:6135195  
A;Accession: S10848  
A;Molecule type: mRNA  
A;Residues: 1-89 <TAT>  
A;Cross-references: EMBL:X02657; NID:g63314; PIDN:CAA26493.1; PID:g63315  
A;Accession: S10480  
A;Molecule type: DNA  
A;Residues: 17-73 <TAW>  
R;Vogeli, G.; Ohkubo, H.; Sobel, M.E.; Yamada, Y.; Pastan, I.; de Crombrughe, B.  
Proc. Natl. Acad. Sci. U.S.A. 78, 5334-5338, 1981  
A;Title: Structure of the promoter for chicken alpha-2 type I collagen gene.  
A;Reference number: S11146; MUID:82060240; PMID:6946474  
A;Accession: S11146  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-15 <VOG>  
R;Yamada, Y.; Avvedimento, V.E.; Mudryj, M.; Ohkubo, H.; Vogeli, G.; Irani, M.; Pastan, Cell 22, 887-892, 1980

A:Title: The collagen gene: evidence for its evolutionary assembly by amplification of a  
A:Reference number: I50170; MUID:81112157; PMID:7460017  
A:Accession: I50628  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 126-161 <YAM>  
A:Cross-references: EMBL:V00400; NID:G63305; PID:G833611  
A:Accession: I50170  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 126-161 <YAZ>  
A:Cross-references: GB:J00828; NID:G211295; PIDN:AAA51612.1; PID:G211317  
A:Accession: I50625  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 530-558 <YAZ>  
A:Cross-references: EMBL:V00396; NID:G63295; PID:G833609  
A:Accession: I50626  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 572-601 <YAA>  
A:Cross-references: EMBL:V00398; NID:G632299; PID:G833610  
A:Accession: I50624  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 433-483 <YAS>  
A:Cross-references: EMBL:V00394; NID:G63287; PID:G833608  
R:Kang, A.H.; Gross, J.  
Biochemistry 9, 796-804, 1970  
A:Title: Amino acid sequence of cyanogen bromide peptides from the amino-terminal region  
A:Reference number: A90568; MUID:70131186; PMID:4313735  
A:Accession: A90568  
A:Molecule type: protein  
A:Residues: 'Z', 79-92 <KAN>  
A:Experimental source: skin  
R:Kang, A.H.; Igarashi, S.; Gross, J.  
Biochemistry 8, 3200-3204, 1969  
A:Title: Characterization of the cyanogen bromide peptides from the alpha2 chain of chick  
A:Reference number: A90557; MUID:69285369; PMID:5809220  
A:Accession: A90557  
A:Molecule type: protein  
A:Residues: 'Z', 79-95; 398-409, 'A', 411, 'V', 413-428 <KAN>  
A:Experimental source: skin  
A:Note: the compositions of the six CNBr peptides were determined. CNBr0 is residues 93-  
R:Highberger, J.H.; Kang, A.H.; Gross, J.  
Biochemistry 10, 610-616, 1971  
A:Title: Comparative studies on the amino acid sequence of the alpha2-CB2 peptides from  
A:Reference number: A90358; MUID:71115216; PMID:5544653  
A:Accession: B90358  
A:Molecule type: protein  
A:Residues: 399-409, 'A', 411, 'V', 413-428 <HIG>  
A:Experimental source: skin  
R:Lane, J.M.; Miller, E.J.  
Biochemistry 8, 2134-2139, 1969  
A:Title: Isolation and characterization of the peptides derived from the alpha2 chain of  
A:Reference number: A90555; MUID:69206882; PMID:5785233  
A:Accession: A90555  
A:Molecule type: protein  
A:Residues: 'Z', 79-95; 398-409, 'A', 411, 'V', 413-428 <LAN>  
A:Experimental source: bone  
A:Note: the compositions of the six CNBr peptides were determined  
A:Note: the compositions of CNBr1, CNBr0, and CNBr2 are identical with those from skin a  
R:Igarashi, S.; Kang, A.H.; Gross, J.  
Biochem. Biophys. Res. Commun. 38, 697-702, 1970  
A:Title: Renaturation and ordering by electron microscopy of the cyanogen bromide peptid  
A:Reference number: A90168; MUID:70181851; PMID:5443711  
A:Contents: annotation; skin, order of CNBr peptides  
R:Vuust, J.; Lane, J.M.; Pietrek, P.P.; Miller, E.J.; Piez, K.A.  
Biochem. Biophys. Res. Commun. 38, 703-708, 1970  
A:Title: The order of the CNBr peptides from the alpha2 chain of collagen.  
A:Reference number: A90169; MUID:70181852; PMID:5443712  
A:Contents: annotation; bone, order of CNBr peptides  
R:Wozney, J.; Hanahan, D.; Tate, V.; Boedtker, H.; Doty, P.

Nature 294, 129-135, 1981  
A:Title: Structure of the pro alpha-2(I) collagen gene.  
A:Reference number: S07327; MUID:82058081; PMID:6272119  
A:Accession: S07327  
A:Molecule type: DNA  
A:Residues: 74-92; 93, 247-431; 432, 693-774 <WZ>  
A:Cross-references: EMBL:J00826  
R:Fuller, F.; Boedtker, H.  
Biochemistry 20, 996-1006, 1981  
A:Title: Sequence determination and analysis of the 3' region of chicken pro-alpha 1(I) c  
A:Reference number: I50623; MUID:81160715; PMID:6927845  
A:Accession: I50623  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 506-830, 'T', 831-903, 'N', 904-964 <FUL>  
A:Cross-references: EMBL:V00390; NID:G63248; PIDN:CAA23688.1; PID:G63249  
R:Avvedimento, E.V.; Vogeli, G.; Yamada, Y.; Maizel, J.V.  
Cell 21, 689-696, 1980  
A:Title: Correlation between splicing sites within an intron and their sequence complemer  
A:Reference number: I50172; MUID:81064671; PMID:6159982  
A:Accession: I50172  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 536-558 <AVV>  
A:Cross-references: GB:M10581; NID:G211323; PIDN:AAA48637.1; PID:G211326  
R:Lehrach, H.; Frischauf, A.M.; Hanahan, D.; Wozney, J.; Fuller, F.; Crkvenjakov, R.; Bo  
Proc. Natl. Acad. Sci. U.S.A. 75, 5417-5421, 1978  
A:Title: Construction and characterization of a 2.5-kilobase procollagen clone.  
A:Reference number: I50171; MUID:79074829; PMID:364479  
A:Accession: I50171  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 484-505 <LEH>  
A:Cross-references: GB:J00837; NID:G4530617; PIDN:AAA51614.1; PID:G211320  
C:Genetics:  
A:Gene: COL1A2  
A:Introns: 24/1; 27/3; 33/3; 45/3; 73/3; 92/3; 107/3; 125/3; 143/3; 161/3; 179/3; 197/3;  
A:Note: the list of introns is incomplete  
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology  
C:Keywords: blocked amino end; coiled coil; extracellular matrix; glycoprotein; hydroxyp  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-77/Domain: amino-terminal propeptide #status predicted <PRO>  
F:78-94/Product: collagen alpha 2(I) chain (fragments) #status predicted <WATN>  
F:78-96/Region: amino-terminal nonhelical telopeptide  
F:737-964/Domain: fibrillar collagen carboxyl-terminal homology <FCC>  
F:78/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone carbo  
F:83/Modified site: allysine (Lys) #status experimental  
F:422,425/Modified site: 4-hydroxyproline (Pro) #status experimental  
F:866/Binding site: carbonylate (Asn) (covalent) #status predicted  
Query Match 9.7%; Score 68.5; DB 1; Length 964;  
Best Local Similarity 31.6%; Pred. No. 87;  
Matches 18; Conservative 6; Mismatches 30; Indels 3; Gaps 1;  
QY 76 VLAFITCLLYALDVVFPQISSVKDKKAVLSDIGVSGFHPAGTPTCTESTGCGCP 132  
DB 9 ILLLLAVTSYLTQSH---VSEASAGRKGRDCKGQGERGPPGPRDGEDGPPGF 62  
RESULT 47  
B71635  
phosphatidylglycerophosphatase A (pgpa) RP750 - Rickettsia prowazekii  
C:Species: Rickettsia prowazekii  
C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, U.  
Nature 396, 133-140, 1998  
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A:Reference number: A71630; MUID:99039499; PMID:9823893  
A:Accession: B71635  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-201 <AND>



F:120/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 9.7%; Score 68; DB 2; Length 618;  
Best Local Similarity 35.7%; Pred. NO. 61;  
Matches 15; Conservative 5; Mismatches 20; Indels 2; Gaps 1;

QY 93 POISSVKDR--KKAFLSDIGVSGEPHPAGTPCTESTEGCGGP 132  
| : || | : | | : | | : | | : | |  
Db 137 PGLQGVKGHAGKRGILGDPGHQKPGPKGDVGASGEQIGGP 178  
| : | | : | | : | | : | | : | |

Search completed: August 11, 2005, 08:24:58  
Job time : 17 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 59 Seconds  
(without alignments)  
1145.669 Million cell updates/sec

Title: US-10-643-836-297

Perfect score: 703

Sequence: 1 MEGGAYGACGAGFDPYTL.....GEPHPAGTCTESTGCGPGP 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Uniprot 03:\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	82.1	234	1 SNG1_HUMAN	O43759 homo sapien
2	550	78.2	234	1 SNG1_MOUSE	O55100 mus musculus
3	547	77.8	234	1 SNG1_RAT	O62876 rattus norv
4	500	71.1	231	2 Q8UW67	Q8UW67 xenopus lae
5	362	51.5	229	1 SNG3_MOUSE	Q8R191 mus musculus
6	353	50.2	229	1 SNG3_HUMAN	O43761 homo sapien
7	306	43.5	219	2 Q6DIE7	O6DIE7 xenopus tro
8	304	43.2	217	2 Q6AZR4	O6AZR4 xenopus lae
9	296	42.1	224	1 SNG2_HUMAN	O43760 homo sapien
10	289.5	41.2	294	2 Q7QHR6	Q7QHR6 anopheles g
11	287	40.8	145	2 Q96L30	Q96L30 homo sapien
12	286	40.7	241	2 Q9V6U3	Q9V6U3 drosophila
13	282	40.1	234	1 SNG2_RAT	O54980 rattus norv
14	274	39.0	224	1 SNG2_MOUSE	O55101 mus musculus
15	274	39.0	224	2 Q8C2Z5	Q8C2Z5 mus musculus
16	274	39.0	224	2 Q99K83	Q99K83 mus musculus
17	211	30.0	191	2 Q6S8H7	Q6S8H7 homo sapien
18	192	27.3	247	1 SNG1_CAEEL	O76735 caenorhabdi
19	170	24.2	233	1 SNG4_MOUSE	O92112 mus musculus
20	169	24.0	234	1 SNG4_HUMAN	O95473 homo sapien
21	167.5	23.8	236	2 Q8E8E8	Q8E8E8 xenopus lae
22	85	12.1	626	2 Q9NHW1	Q9NHW1 nephila ina
23	84.5	12.0	235	2 Q6PEJ1	Q6PEJ1 brachydanio
24	82.5	11.7	202	2 Q8S3G7	Q8S3G7 mycobacteri
25	82	11.7	462	2 Q3NHX3	Q3NHX3 nephila cla
26	82	11.7	907	2 Q443S9	Q443S9 nephila cla
27	81.5	11.6	161	2 Q2KDP9	Q2KDP9 rhizobium m
28	80	11.4	468	1 PTMB_BACHD	Q9K678 bacillus ha
29	79.5	11.3	538	2 Q8H4H5	Q8H4H5 oryza sativ
30	78	11.1	392	1 GOST_CHICK	P28337 gallus gall
31	77.5	11.0	650	2 Q6LKE4	Q6LKE4 photobacter

#### RESULT 1

SNG1\_HUMAN STANDARD; PRT; 234 AA.  
 AC O43759; O43757; O43758; Q96J56; Q9UGZ4;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Synaptogyrin-1.  
 GN Name=SYNGR1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98430994; PubMed=9760194;  
 RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,  
 RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,  
 RA Dumanski J.P.;  
 RT "Characterization of the human synaptogyrin gene family.";  
 RL Hum. Genet. 103:131-141(1998).  
 RN [2]  
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 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;  
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,  
 RA Clamp M., Slink L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
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 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
 RA Clegg S.M., Colby V.E., Cole C.G., Collier R.E., Connor R.,  
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
 RA Dharm D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
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 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,  
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
 RA Hunt S.E., Jones M.C., Kersey J., Kimberley A.M., King A.,  
 RA Laird G.K., Langford C.F., Levensha M.A., Lloyd C., Lloyd D.M.,  
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
 RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Minoshima S., Asakawa K., Sasaki T., Asakawa S., Kudo J.,  
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

#### ALIGNMENTS

32	76	10.8	251	2	Q7ZNV8
33	76	10.8	288	2	Q6ZM74
34	76	10.8	439	2	Q731J4
35	76	10.8	519	2	Q7NFW8
36	75.5	10.7	232	2	Q6TLG1
37	75.5	10.7	348	1	Y479_MYCTU
38	75.5	10.7	348	1	Y489_MYCBO
39	75.5	10.7	460	2	Q6P2P0
40	75.5	10.7	530	1	MATP_HUMAN
41	75	10.7	249	2	Q946I4
42	75	10.7	249	2	Q7G6Z4
43	75	10.7	439	2	Q635H8
44	75	10.7	439	2	Q818Y3
45	75	10.7	439	2	Q81MC4
46	75	10.7	439	2	Q6HE62
47	75	10.7	667	2	Q8VUH1
48	75	10.7	760	2	Q6BLQ5
49	74.5	10.6	533	2	Q73FF3
50	74.5	10.6	533	2	Q81VY5

Q7ZNV8 xenopus lae  
 Q6ZM74 brachydanio  
 Q731J4 bacillus ce  
 Q7NFW8 gloebacter  
 Q6TLG1 brachydanio  
 P64699 mycobacteri  
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 Q6P2P0 homo sapien  
 Q946I4 oryza sativ  
 Q7G6Z4 oryza sativ  
 Q635H8 bacillus ce  
 Q818Y3 bacillus ce  
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 Q6HE62 bacillus th  
 Q8VUH1 streptococ  
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 Q73FF3 bacillus ce  
 Q81VY5 bacillus an



RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
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RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
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RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,  
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,  
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
RA Peyraud M., Kedra D., Serousi E., Fransson I., Tapia I., Bruder C.E.,  
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
RA Khan A.S., Lane L., Tiliahun Y., Wright H.,  
RA "The DNA sequence of human chromosome 22";  
RL Nature 402:489-495(1999).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1B).  
RC TISSUE=Brain;  
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickens M.C.,  
RA Rodriguez A.C., Gromwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1A;  
CC IsoId=O43759-1; Sequence=displayed;  
CC Name=1B;  
CC IsoId=O43759-2; Sequence=VSP\_006332;  
CC Name=1C;  
CC IsoId=O43759-3; Sequence=VSP\_006331, VSP\_006332;  
CC -!- SIMILARITY: Belongs to the synaptogyrin family.  
CC -----  
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CC -----  
CC EMBL; AJ002305; CAA05322.1; -  
CC EMBL; AJ002304; CAA05321.1; -  
CC EMBL; AJ002303; CAA05320.1; -  
CC EMBL; AL022326; CAA18451.1; -  
CC EMBL; AL022326; CAA18452.1; -  
CC EMBL; AL022326; CAA18453.1; -  
CC EMBL; BC000731; AAH00731.1; -  
CC Genew; HGNC:11498; SYNGRI.  
CC H-InvDB; HIX0016490; -  
CC MIM; 603925; -  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC InterPro; IPR008253; Marvel.

DR Pfam; PF01284; MARVEL; 1.  
KW Alternative splicing; Synapse; Transmembrane.  
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FT TRANSMEM 72 92 Potential.  
FT TRANSMEM 104 124 Potential.  
FT TRANSMEM 149 169 Potential.  
FT VARSPLIC 1 33  
FT MEGGAGAGKAGGAFDPYTLVRQPHILRVSW -> MLTL  
FT EFGILEPDPSPGSMGTSQTSRWSRSPGCE (in  
FT isoform 1C).  
FT /FTId=VSP\_006331.  
FT AGQAVLAQRQVIGADSAALFSDYNDPQSDSMPYAPYVEP  
FT NTGPDAGMGTYQQPANTFTPEQGYOQGY -> SLTAA  
FT LAVRRFKDLSFOEYSTLFPASAQ (in isoform 1B  
FT and isoform 1C).  
FT /FTId=VSP\_006332.  
FT Missing (in Ref. 2).  
FT CONFLICT 203 203  
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QY 61 YNRNPACSYGVAVGLAFLTCLLYLALDVVFPQISSVKORKKAVLSDIGVS 112  
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AC 055100; Q9DCB0;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Synaptogyrin-1.  
GN Name=Syngr1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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RN [1]\_TaxID=10090;  
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RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,  
RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,  
RA Dumanski J.P.;  
RT "Characterization of the human synaptogyrin gene family.";  
RL Hum. Genet. 103:131-141(1998).  
RN [2]  
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RC STRAIN=C57BL/6J; TISSUE=Brain;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaudo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Draganl T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,



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[1]
RN      SEQUENCE FROM N.A.
RP      MEDLINE=96134029; PubMed=8557746; DOI=10.1083/jcb.131.6.1801;
RX      Stenius K., Janz R., Suedhof T.C., Jahn R.;
RA      "Structure of synaptogyrin (p29) defines novel synaptic vesicle
RT      protein.";
RL      J. Cell Biol. 131:1801-1809(1995).
RC      CC
CC      CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      CC -2- TISSUE SPECIFICITY: Nervous system.
CC      CC -3- SIMILARITY: Belongs to the synaptogyrin family.
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DR      EMBL; U39549; AAB17890.1; -
DR      RGD; 3801; Syngri1
DR      InterPro; IPR008253; Marvel.
DR      Pfam; PF01284; MARVEL; 1.
DR      KW Synapse; Transmembrane.
FT      TRANSMEM 24 44 Potential.
FT      TRANSMEM 72 92 Potential.
FT      TRANSMEM 105 125 Potential.
FT      TRANSMEM 149 169 Potential.
SQ      SEQUENCE 234 AA; 25669 MW; B3038B64C49F31E1 CRC64;
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Query Match 77.8%; Score 547; DB 1; Length 234;
Best Local Similarity 92.9%; Pred. No. 1-2e-43;
Matches 104; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 MEGGAYGAGKAGGAPDPYTLVRPHTILRVSMLEFSIVFGSIVNEGVLNNSASGEQPCI 60
DB      |||
DB      1 MEGGAYGAGKAGGAPDPYTLVRPHTILRVSMLEFSIVFGSIVNEGVLNNSASGEQPCI 60
-----
QY      61 YNRPNACSYGVAVGLAFITCLLYLALDVFYFQISSVKDKKAVLSDIGVS 112
DB      |||
DB      61 YNRPNACSYGVAVGLAFITCLLYLALDVFYFQISSVKDKKAVLSDIGVS 112
-----
RESULT 4
ID      Q8UW67 PRELIMINARY; PRT; 231 AA.
ID      AC Q8UW67;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      P7D11.
OS      Name=P7D11;
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
ON      [1]
ON      SEQUENCE FROM N.A.
RX      MEDLINE=91643879; PubMed=11784032; DOI=10.1006/dbio.2001.0428;
RA      Shibata M., Itoh M., Ohmori S., Shinga J., Taira M.;
RT      "Systematic screening and expression analysis of the head organizer
RT      genes in Xenopus embryos.";
RL      Dev. Biol. 239:241-256(2001).
DR      EMBL; AB072005; BAB79596.1; -
DR      GO; GO:0016020; C:membrane; IEA..
DR      Pfam; PF01284; MARVEL; 1.
SQ      SEQUENCE 231 AA; 25535 MW; 03982F903EBE3F14 CRC64;
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Query Match 71.1%; Score 500; DB 2; Length 231;
Best Local Similarity 81.2%; Pred. No. 3.3e-39;
Matches 91; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MEGGAYGAGKAGGAFDPYTLVROPHITLRVWSLFSIVVFGSVINVEGYNSASEGEQFCI 60
DB 1 MEGGAYGAGKAGGAFDPQFIQPHITLRVWSLFSIVVFGSVINVEGYNSASEGEHCCI 60
QY 61 YNRNPACSGYVAVGVLAFLTLCLLYLALDVYFPQISSVKDRKAVLSDIGVS 112
DB 61 FNRNPACSGYVAVGVLAFLTLCLLYLALDVYFPQISSVKDRKAVLSDIGVS 112

RESULT 5
SNG3 MOUSE
ID SNG3 MOUSE STANDARD; PRT; 229 AA.
AC Q8R191; Q9WV8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Synaptogyrin-3.
GN Name=Syngr3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315823; PubMed=10383386; DOI=10.1074/jbc.274.27.18893;
RA Sugita S., Janz R., Suedhof T.C.;
RT "Synaptogyrins regulate Ca2+-dependent exocytosis in PC12 cells.";
RL J. Biol. Chem. 274:18893-18901(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Numaiz L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima I., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Iotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to the synaptogyrin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC -----
CC EMBL; AF117207; AAD28556.1; -
CC EMBL; AK048753; BAC33444.1; -
CC EMBL; AK081164; BAC38151.1; -
CC EMBL; AK082167; BAC38430.1; -
CC EMBL; BC025022; AAH25022.1; -
CC MGD; MGI:1341881; Syngr3.
CC DR InterPro; IPR008253; Marvel.
CC DR Pfam; PF01284; MARVEL; 1.
CC KW Transmembrane
CC FT TRANSMEM 30 50 Potential.
CC FT TRANSMEM 70 90 Potential.
CC FT TRANSMEM 105 125 Potential.
CC FT TRANSMEM 148 168 Potential.
CC FT CONFLICT 171 171 F -> L (in Ref. 1).
CC SQ SEQUENCE 229 AA; 24561 MW; E04C00555B8A3C08 CRC64;
Query Match 51.5%; Score 362; DB 1; Length 229;
Best Local Similarity 59.3%; Pred. No. 3.7e-26;
Matches 67; Conservative 20; Mismatches 26; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPYTLVROPHITLRVWSLFSIVVFGSVINVEGYNSASEGEQFCI 60
DB 1 MEGGAYGAGKAGGAFDPVSVFARRPQTLRVVSWVFSIAVFGPIVNEGYNSDGPRLRCV 60
QY 61 YNRNPACSGYVAVGVLAFLTLCLLYLALDVYFPQISSVKDRKAVLSDIGVS 113
DB 61 FNRNPACSGYVAVGVLAFLTLCLLYLALDVYFPQISSVKDRKAVLSDIGVS 113

RESULT 6
SNG3 HUMAN
ID SNG3 HUMAN STANDARD; PRT; 229 AA.
AC Q43761;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-3.
GN Name=SYNGR3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98430994; PubMed=9760194;
RA Kedra D., Fan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
RA Collins J.B., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dumanski J.P.;
RT "Characterization of the human synaptogyrin gene family.";
RL Hum. Genet. 103:131-141(1998).
```

[2]
 RN REVISIONS.
 RP Kedra D.,
 RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RL SEQUENCE FROM N.A.
 [3]
 RN MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RC TISSUE=B-cell;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- TISSUE SPECIFICITY: Expressed in brain and placenta.
 CC -|- SIMILARITY: Belongs to the synaptogyrin family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ002309; CAA05326.2; -.
 DR EMBL; BC014087; AAH14087.1; -.
 DR Genew; HGNC:11501; SYNGR3.
 DR H-InvDB; HIX0012708; -.
 DR MIM; 603927; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR InterPro; IPR008253; Marvel.
 DR Pfam; PF01284; MARVEL; 1.
 DR Transmembrane.
 KW TRANSMEM 30 50 Potential.
 FT TRANSMEM 70 90 Potential.
 FT TRANSMEM 105 125 Potential.
 FT TRANSMEM 148 168 Potential.
 SQ SEQUENCE 229 AA; 24555 MW; 0755812EDD4AD4C5 CRC64;
 Query Match 50.2%; Score 353; DB 1; Length 229;
 Best Local Similarity 58.4%; Pred. No. 2.6e-25;
 Matches 66; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
 QY 1 MEGAGYAGKAGGAGFDPVTLVRQPHTLIRVSVLFSIVFGSIIVNEGVLNSASGEQFCI 60
 DB 1 MEGASGAGRAGAAALDPVSPFARRQTLIRVASVWFSIAVFGPIIVNEGVLNDSGPELRVCV 60
 QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVFYFQISSVKDKKXAVLSDIGVSG 113
 DB 61 FNGNAGACRFVGLGLGFLACAAFLLLDVRFFQISSVRRERRAVLLDLGFSG 113
 RESULT 7
 ID Q6DIE7 PRELIMINARY; PRT; 219 AA.
 AC Q6DIE7
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 GN Name=syngnr2-prov;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI\_TaxID=8364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC075595; AAH75595.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008253; Marvel.
 DR Pfam; PF01284; MARVEL; 1.
 SQ SEQUENCE 219 AA; 24372 MW; 93C4618D9CEFA542 CRC64;
 Query Match 43.5%; Score 306; DB 2; Length 219;
 Best Local Similarity 49.1%; Pred. No. 7e-21;
 Matches 55; Conservative 25; Mismatches 32; Indels 0; Gaps 0;
 QY 1 MEGGAYGAGKAGGAGFDPVTLVRQPHTLIRVSVLFSIVFGSIIVNEGVLNSASGEQFCI 60
 DB 1 MEGSAYGAPKAGGGSFSLNFKRPETILRIISCFALIVFACIVSDGYTNIPNESKLTCI 60
 QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVFYFQISSVKDKKXAVLSDIGVS 112
 DB 61 FKNKNDACHYGVGIGFLACILFLFLDLYLQTLNANYRKIVLADLGFS 112
 RESULT 8
 ID Q6AZR4 PRELIMINARY; PRT; 217 AA.
 AC Q6AZR4
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Syngnr2-prov protein.
 GN Name=syngnr2-prov;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI\_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.



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SQ SEQUENCE 224 AA; 24810 MW; EC92C95CE9E5BD41 CRC64;
Query Match 42.1%; Score 296; DB 1; Length 224;
Best Local Similarity 48.6%; Pred. No. 6.4e-20;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVSWLFSIVVFGSIVNEGYNLSASEGEQFCI 60
DB 1 MESGAYGAAGKAGSFDRLRFLLTQPVQVARVCLVFLVIFVFCYIGGYSNAHESKQMYCV 60

QY 61 YNRNPNCAGSYGAVGVLAFLTCLLYLALDVYFPQISSVDRKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLWVDAFPQISNATDRKYLVIQDL 109

RESULT 10
ID Q7QHR6 PRELIMINARY; PRT; 294 AA.
AC Q7QHR6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE AgCP7107 (Fragment)
GN Name=agCG48315; ORFNames=ENSANGG00000015977;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05258.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; MARVEL.
DR Pfam; PF01284; MARVEL; 1.
FT NON TER 1
SQ SEQUENCE 294 AA; 33098 MW; 4671F09266A3C730 CRC64;

Query Match 41.2%; Score 289.5; DB 2; Length 294;
Best Local Similarity 42.9%; Pred. No. 3.4e-19;
Matches 60; Conservative 21; Mismatches 28; Indels 31; Gaps 2;

QY 3 GGAYGAGKAGGAFDPYTLVRQPHILRVVSW----- 33
DB 21 GGAYGGKAGGAFDPPIAFVQRPVTLRAVCWVSLAGEQNCPPFPKDTLFPKYLQCV 80

QY 34 -LFSIVVFGSIVNEGYNLSASEGEQFCIYNRNPNCAGSYGAVGVLAFLTCLLYLALDVYF 92
DB 81 PLFAIIIVFGCISSEGWEAN-GKEYCTIIRDGACNACVAVGIGVIAFLAAMGFIAEYLF 139

QY 93 PQISSVDRKAVLSDIGVS 112
DB 140 EQMSSVTRKHVYLAIDIGFS 159

RESULT 11
ID Q96L30 PRELIMINARY; PRT; 145 AA.
AC Q96L30;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SYNGR3 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
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```
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 12;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009568; AAH09568.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; MARVEL.
DR Pfam; PF01284; MARVEL; 1.
SQ SEQUENCE 145 AA; 15164 MW; A23BE7A9BC953CA3 CRC64;

Query Match 40.8%; Score 287; DB 2; Length 145;
Best Local Similarity 56.4%; Pred. No. 3e-19;
Matches 53; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVSWLFSIVVFGSIVNEGYNLSASEGEQFCI 60
DB 1 MEGAGFGAGRGAAGALDPVSFARFQTLRLVASVFSIAVFGPIVNEGYNVNTSGPELRV 60

QY 61 YNRNPNCAGSYGAVGVLAFLTCLLYLALDVYFPQ 94
DB 61 FNGNAGACRFGVALGLGAFACAAFLLLDVRFOQ 94

RESULT 12
ID Q9V6U3 PRELIMINARY; PRT; 241 AA.
AC Q9V6U3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 23-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG10808-PA (RH60941p).
GN Name=synaptogyrin; ORFNames=CG10808;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.K., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodagett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RL a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RN
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RN
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[7]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003817; AAF58329.1; -
DR EMBL; AY071753; AAL49375.1; -
DR FlyBase; FBgn0033876; synaptogyrin.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
SQ SEQUENCE 241 AA; 26610 MW; CFCBDA1D44450E86A CRC64;
Query Match 40.7%; Score 286; DB 2; Length 241;
Best Local Similarity 47.3%; Pred. No. 6e-19;
Matches 52; Conservative 24; Mismatches 32; Indels 2; Gaps 1;
QY 3 CGAYGAGKAGGAFDPYTLVRQPHHTLRLVVSMLFSLVVGSIYVNGVLSASGEQFCIYN 62
DB 13 GGAYGGKAGGAFDPLTFAMKQVVRALCWLFSSVVGISSEGW--TEKDGKEYCLYN 70
QY 63 RNPNACSYGVAVGVLAFLLTLVLDVVFQISSLVVDKDKKAVLSDIGVS 112
DB 71 GPGMACKGNMVGVGFLASMGFMGGEFLFERMSSVSKSRKYVMADMGSF 120
RESULT 13
SNG2 RAT STANDARD; PRT; 234 AA.
AC O54980;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-2 (Cellugyrin).
GN Name-Syngtr2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112834; PubMed=9446595; DOI=10.1074/jbc.273.5.2851;
RA Janz R., Suedhof T.C.;
RT "Cellugyrin, a novel ubiquitous form of synaptogyrin that is
RL phosphorylated by pp60(c-src).";
RL J. Biol. Chem. 273:2851-2857(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Ubiquitous, low expression in brain.
CC -!- PTM: Tyrosine phosphorylated by Src.
CC -!- SIMILARITY: Belongs to the synaptogyrin family.
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CC -----
CC EMBL; AF039085; AAB96666.1; --
CC RGD; 621334; Syngtr2.
CC InterPro; IPR008253; Marvel.
CC Pfam; PF01284; MARVEL; 1.
KW Phosphorylation; Transmembrane.
FT TRANSMEM 40 60 Potential.
FT TRANSMEM 83 103 Potential.
FT TRANSMEM 115 135 Potential.
FT TRANSMEM 157 177 Potential.
SQ SEQUENCE 234 AA; 25709 MW; 68168A78CCF5B8C CRC64;
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RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089424; BAC0876.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
SQ SEQUENCE 224 AA; 24759 MW; 950B5F503729AF0C CRC64;

Query Match 39.0%; Score 274; DB 2; Length 224;
Best Local Similarity 45.0%; Pred. No. 7.7e-18;
Matches 49; Conservative 22; Mismatches 38; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGADPYTLVRQPHITLVRVSWLFSIVVFGSIVNEGYNLSASEGEGQFCI 60
Db 1 MESGAYGANAGGSFDLRRFLSQPVQVTRLVSVLALIVFSCIFGEGYNIHTSDQLYCV 60
QY 61 YNRNPNCAGSYGAVGVLAFLTCLLYLALDVVFPQISSVKDRKKAVLSDI 109
Db 61 FNQNEADACHYSAIGVLAFLASAFFLVVDFAFQSQISNATDRKYLVIIGDL 109

RESULT 16
Q99K83 PRELIMINARY; PRT; 224 AA.
AC Q99K83;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Syngt2 protein.
GN Name=Syngt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausberg R.L., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004829; AAH04829.1; -.
DR MGD; MGI:1328324; Syngt2.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
SQ SEQUENCE 224 AA; 24790 MW; 9505C914C9C3EEB6 CRC64;

Query Match 39.0%; Score 274; DB 2; Length 224;
Best Local Similarity 45.0%; Pred. No. 7.7e-18;
Matches 49; Conservative 22; Mismatches 38; Indels 0; Gaps 0;

RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089424; BAC0876.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
SQ SEQUENCE 224 AA; 24759 MW; 950B5F503729AF0C CRC64;

Query Match 39.0%; Score 211; DB 2; Length 191;
Best Local Similarity 47.4%; Pred. No. 6e-12;
Matches 36; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 34 LFSIVVFGSIVNEGYNLSASEGEGQFCIVNRPNCAGSYGAVGVLAFLTCLLYLALDVVPP 93
Db 1 VFALIVFSCIYEGYSNAHESQKQYCVFNREDACRYGSAIGVLAFLASAFFLVVDAYFP 60
QY 94 QISSVKDRKKAVLSDI 109
Db 61 QISNATDRKYLVIIGDL 76

RESULT 18
SNG1_CAEEL STANDARD; PRT; 247 AA.
ID SNG1_CAEEL
AC 076735; Q22340;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin homolog 1.
GN Name=sg-1; ORFNames=T08A9.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nonet M.;
RT "Visualization of presynaptic terminal specializations in live C.
elegans with synaptic vesicle protein-GFP fusions.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
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QY 21 VROPHTILRVWSLFSIVVFGSVNGLNSASEGQFCIYNPNACSVGVAVGLAFL 80
Db 19 LRRPKSIRIFGVSILVIFSSLLTDGYQNTSPQLRCVLNSHNWACSFVAGGFLSEL 78
QY 81 TCLLYLALDVY 91
Db 79 SCLVFLAIDAY 89

RESULT 20
ID _SNG4 HUMAN STANDARD; PRT; 234 AA.
AC Q95473;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-4.
GN Name=SYNGR4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kedra D., Dmanski J.P.;
RT "Cloning of a novel member of synaptogyrin gene family.";
RL Submitted (Oct-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the synaptogyrin family.
CC -----
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CC -----
DR EMBL; AJ011733; CAA09754.1; -.
DR Genew; HGNC:11502; SYNGR4.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KW Transmembrane.
FT TRANSMEM 25 45 Potential.
FT TRANSMEM 66 86 Potential.
FT TRANSMEM 104 124 Potential.
FT TRANSMEM 145 165 Potential.
SQ SEQUENCE 234 AA; 25786 MW; 801134E4D840288F CRC64;

Query Match 24.0%; Score 169; DB 1; Length 234;
Best Local Similarity 38.6%; Pred. No. 6.9e-08;
Matches 34; Conservative 16; Mismatches 38; Indels 0; Gaps 0;

QY 21 VROPHTILRVWSLFSIVVFGSVNGLNSASEGQFCIYNPNACSVGVAVGLAFL 80
Db 19 LRRPKTIRTFEGVFSILVIFSSLLTDGYQNMESPOLRCILNSVACSFVAGGFLAFL 78
QY 81 TCLLYLALDVYFPQISVKDKKAVLSD 108
Db 79 SCLAVLDTQETRIAGTRKTAFLD 106

RESULT 21
ID Q68ES8 PRELIMINARY; PRT; 236 AA.
AC Q68ES8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE LOC446291 protein (Fragment).
GN Names=LOC446291;
OS Xenopus laevis (African clawed frog).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RX Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC080122; AAH80122.1; -.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
FT NON_TER 1
SQ SEQUENCE 236 AA; 25738 MW; C1AE117F82DEAA7C CRC64;

Query Match 23.8%; Score 167.5; DB 2; Length 236;
Best Local Similarity 34.3%; Pred. No. 9.6e-08;
Matches 37; Conservative 20; Mismatches 46; Indels 5; Gaps 1;

QY 6 YGAGKAGGAFDPYTLVROPHTILRVWSLFSIVVFGSVNGLNSASEGQFCIYNRNP 65
Db 9 FSAKSGAPSGLVDFIRFPVILRLSSILTSIIVGAV-----SSGCKTHDVCIFNGS 63
QY 66 NCCTGVAVGVLAFLTCLLYLALDVYFPQISVKDKKAVLSDIGVSG 113
Db 64 SPCSCLAVAIQVFAFLGSVAFVDSYFNFSISNKKRRRVYVMGDLAFSG 111

RESULT 22
ID Q9NHW1 PRELIMINARY; PRT; 626 AA.
AC Q9NHW1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Flagelliform silk protein (Fragment).
GN Name=Flag;
OS Nephila inaurata madagascariensis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneoidae; Tetragnathidae; Nephila.
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DR GO:0016020; C:membrane; IEA.  
DR GO:0008021; C:synaptic vesicle; IEA.  
DR GO:0009215; F:transporter activity; IEA.  
DR GO:0006810; P:transpor; IEA.  
DR InterPro; IPR008253; Marvel.  
DR pfam; PF01284; MARVEL; 1.  
DR PRINTS; PR00220; SYNAPTOPHYSN.  
KW Hypochemical protein.  
SQ SEQUENCE 235 AA; 26152 MW; 86C1F0EDA2998B48 CRC64;  
  
Query Match      12.0%; Score 84.5; DB 2; Length 235;  
Best Local Similarity 21.9%; Pred.No.6-9;  
Matches 28; Conservative 26; Mismatches 35; Indels 39; Gaps 5;  
  
QY    21 VROPHTILRVVSLFSIVVFSGIINVEGYLNS-----ASGEQP----- 58  
       |||:||||::|::|::|::|::|::|::|::|::|::|:  
Db     18 VKPEPLGFIRLLWVFITCAFAT--TGGYGVSFTVLTKCPDKDVDVTANFYPPRLPSHP 75  
  
QY    59 -----CIYNRN-----PNACSYGVAGVLAFLCLLLALDVVPFOISSVKRKKAV 105  
       ::|::|::|::|::|::|::|::|::|::|::|::|:  
Db     76 YLINHGNGSNNTTYLOGDFSSSAEFFSVISGLVGLEYCTFTLLLYLGQQV--YRESNRGP 133  
  
QY    106 LSDIGVSG 113  
       :|::|::|:  
Db     134 IIDLVGTG 141  
  
RESULT 24  
Q853G7 PRELIMINARY;   PRT;   202 AA.  
ID Q853G7  
AC Q853G7; 2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DI 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Gpl14.  
DS  
GN Names=114;  
OS Mycobacteriophage Bxzl.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.  
OX NCBI_TaxID=205877;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;  
RA Pedulla M.L., Ford M.E., Houtz J.M., Kartikeyan T., Wadsworth C.,  
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,  
RA Brucker W., Kumar V., Kandasamy J.J., Keenan L., Bardarov S.,  
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,  
RA Hatfull G.F.;  
RA "Origins of highly mosaic mycobacteriophage genomes.";  
RL Cell 113:171-182(2003).  
RE EMBL; AY129337; ANNI6770.1; -.  
DR InterPro; IPR008972; Cupredoxin.  
SQ SEQUENCE 202 AA; 21082 MW; DC82F1993B89BF55 CRC64;  
  
Query Match      11.7%; Score 82.5; DB 2; Length 202;  
Best Local Similarity 30.2%; Pred.No.9.1;  
Matches 32; Conservative 9; Mismatches 42; Indels 23; Gaps 5;  
  
QY    45 NEGYLNASGEQCICV-----NRNPACSVC-GVAV-----GVLAFLTCLLYL--- 86  
       |::|::|::|::|::|::|::|::|::|::|::|:  
Db     16 NPGHITIIVEGESIVVMQSQNPNPHEPTCTIAGSVPLIQDLINGSLSINTYCFCALLNPP 75  
  
QY    87 ---ALDYVFFQISSVKDRKXAVSDIGVSGEP--HPAGTPCTESTE 127  
       |||::|::|::|::|::|::|::|::|::|::|::|:  
Db     76 VGTDLAVAFPVIGSYDAACTIVLKGVGSGFGTFPVQHITTKKSITASTE 121  
  
RESULT 25  
Q9NHW3 PRELIMINARY;   PRT;   462 AA.  
ID Q9NHW3  
AC Q9NHW3,  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
```

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Flagelliform silk protein (Fragment).
GN Name=Flag;
OS Nephila clavipes (Orb spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Tetragnathidae; Nephila.
OX NCBI_TaxID=6915;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20156786; PubMed=10688794; DOI=10.1126/science.287.5457.1477;
RA Hayashi C.Y., Lewis R.V.;
RT "Molecular architecture and evolution of a modular spider silk protein
   gene.";
RL Science 287:1477-1479 (2000).
DR ENBL; AF218622; AAF36089.1; -.
FT NON_TER 1 1
FT NON_TER 462 462
SQ SEQUENCE 462 AA; 38393 MW; 31DF2549C4CFC285 CRC64;

Query Match 11.7%; Score 82; DB 2; Length 462;
Best Local Similarity 32.9%; Pred. No. 23;
Matches 28; Conservative 14; Mismatches 27; Indels 16; Gaps 5;

QY 3 GGAYGAGKAGAPDPTLVQRPHILRVSWL----FSIVVFGSIYNEGVLNLSASGEQF 58
   ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 368 GGAYGFGPGGAYYPS--RVPDMVNGIMSGGFGFYQMFQNM-----LSQYSSSGST 420

QY 59 CIYNRNPNACSYGVAVGVLAFLTCL 83
   | | | | : : : : : : : : : : : : : : : : : : : : : : : :
DB 421 C-----NPNNVNV-LMDALLAALHCL 440

RESULT 26
O44359 PRELIMINARY; PRT; 907 AA.
AC O44359;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Flagelliform silk protein (Fragment).
GN Name=Flag;
OS Nephila clavipes (Orb spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Tetragnathidae; Nephila.
OX NCBI_TaxID=6915;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98153262; PubMed=9480769; DOI=10.1006/jmbi.1997.1478;
RA Hayashi C.Y., Lewis R.V.;
RT "Evidence from flagelliform silk cDNA for the structural basis of
   elasticity and modular nature of spider silks.";
RL J. Mol. Biol. 275:773-784 (1998).
DR ENBL; AF027973; AAC38847.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008160; Collagen.
FT NON_TER 1 1
SQ SEQUENCE 907 AA; 72992 MW; A0864EC708740A00 CRC64;

Query Match 11.7%; Score 82; DB 2; Length 907;
Best Local Similarity 32.9%; Pred. No. 24;
Matches 28; Conservative 14; Mismatches 27; Indels 16; Gaps 5;

QY 3 GGAYGAGKAGAPDPTLVQRPHILRVSWL----FSIVVFGSIYNEGVLNLSASGEQF 58
   ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 805 GGAYGPGSPGAYYPS--RVPDMVNGIMSGGFGFYQMFQNM-----LSQYSSSGST 857

QY 59 CIYNRNPNACSYGVAVGVLAFLTCL 83
   | | | | : : : : : : : : : : : : : : : : : : : : : : : :
DB 858 C-----NPNNVNV-LMDALLAALHCL 877

RESULT 27
```

```
Q92KD9 PRELIMINARY; PRT; 161 AA.
ID Q92KD9;
AC Q92KD9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HYPOTHETICAL TRANSMEMBRANE PROTEIN.
GN OREName=SMC01024;
OS Rhizobium melliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godelle T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
   Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
DR EMBL; AL591787; CAC46018.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015450; F:protein translocase activity; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR004692; SecG.
DR Pfam; PF03840; SecG; 1.
DR PRINTS; PR01651; SECSEXPORT.
DR TIGRfams; TIGR00810; secG; 1.
KW Complete proteome; Hypothetical protein; Transmembrane.
SQ SEQUENCE 161 AA; 15322 MW; 73459FBE862BCEFC CRC64;

Query Match 11.6%; Score 81.5; DB 2; Length 161;
Best Local Similarity 30.5%; Pred. No. 9.1;
Matches 32; Conservative 14; Mismatches 46; Indels 13; Gaps 4;

QY 26 TILRVVSWLFSIVFGSIV---NEGVLNLSASGEQFCIYNRNPNACSYGVAVGVLAFLTC 82
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 3 TVLLVIYLMVVVALIGVLIQISGGLGIGGGSGFMSARGTANALTRTTA--VLAFLFF 60

QY 83 LLYVLAADV---YFPOISSVKDRKKAVLSDIGV-----SGEPHPAG 119
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 61 ALALANGILSRYPQATDILDRIPGTSSTSGGVLDLSLGGGQPAPAG 105

RESULT 28
PTMB_BACHD
ID PTMB_BACHD STANDARD; PRT; 468 AA.
AC Q9K678;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE PTS system, mannitol-specific IIBC component (EIIBC-Mtl) (Mannitol-
DE permease IIBC component) (Phosphotransferase enzyme II, BC component)
DE (EC 2.7.1.69) (EIIBC-Mtl).
GN Name=mtIIA; OrderedLocusNames=BH3854;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
CC -!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
```

sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPr); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to the sugar (By similarity).

CC -I- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphate.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -I- SIMILARITY: Contains 1 PTS EIIIC domain.

CC -I- SIMILARITY: Contains 1 PTS EIIIC domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; AP001520; BAB07573.1; -

DR PIR; F84131; F84131.

DR InterPro; IPR003352; Ptrans\_EIIC.

DR InterPro; IPR003501; Ptrans\_IIB.

DR InterPro; IPR004718; PTSIIC\_mtla.

DR Pfam; PF02378; PTS\_EIIC; 1.

DR Pfam; PF02302; PTS\_IIB; 1.

DR TIGRfams; TIGR00851; mtla; 1.

DR Complete proteome; Phosphorylation; Phosphotransferase system; KW Sugar transport; Transferase; Transmembrane.

FT DOMAIN 1 335 EIIC.

FT TRANSMEM 336 468 Potential.

FT TRANSMEM 20 40 Potential.

FT TRANSMEM 50 70 Potential.

FT TRANSMEM 93 113 Potential.

FT TRANSMEM 137 157 Potential.

FT TRANSMEM 163 183 Potential.

FT TRANSMEM 215 235 Potential.

FT TRANSMEM 269 289 Potential.

FT TRANSMEM 290 310 Potential.

FT TRANSMEM 316 336 Potential.

FT MOD RES 258 258 Phosphohistidine (By similarity).

FT MOD RES 386 386 Phosphocysteine (By similarity).

SQ SEQUENCE 468 AA; 49037 MW; 7B0FDA747E75DEB8 CRC64;

Query Match 11.4%; Score 80; DB 1; Length 468;

Best Local Similarity 28.1%; Pred. No. 36;

Matches 36; Conservative 13; Mismatches 49; Indels 30; Gaps 6;

QY 11 AGGAFD---PYTLVROPHITLTVV---SMLFSTVVFSGSVNGLNSAGEQFCIYNR 63

Db 254 AGGIHETFPYILMK-PTLILAVTAGMSGVFTFLV---NAGLVAVPFGSIFALLAM 308

QY 64 NPNAACSYGAVGVLAFLTCLLYLALDYVFPQISSVKDRKAVLSDIGVSGEPHPAGPCT 123

Db 309 TPREGYAGLVGI-----IATVSVFIASIIKTSKATADL-----TEAT 350

QY 124 ESTEGCPG 131

Db 351 SKMEGLKG 358

RESULT 29

Q8H4H5 PRELIMINARY; PRT; 538 AA.

AC Q8H4H5;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Putative Nrampl protein (Putative NRAMPL-like protein).

GN Name=QJ1057\_E05.110; Synonyms=Nrampl;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI\_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Yamamoto K.,

RT "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 7, BAC clone:OJ1057\_E05.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Gross J., Stein R.J., Fett-Neto A.G., Fett J.P.;

RT "Iron homeostasis related genes in rice.";

RL Genet. Mol. Biol. 26:477-497(2003).

DR EMBL; AP004176; BAC21413.1; -

DR EMBL; BK000593; DAA01394.1; -

DR Gramene; Q8H4H5; -

DR GO; GO:0016020; C-membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001046; Nrampl.

DR Pfam; PF01566; Nrampl; 1.

DR PRINTS; PR00447; NATRESASSCMP.

DR ProDom; PD001861; Nrampl; 1.

DR TIGRfams; TIGR01197; nrampl; 1.

SQ SEQUENCE 538 AA; 58497 MW; B07763D611234327 CRC64;

Query Match 11.3%; Score 79.5; DB 2; Length 538;

Best Local Similarity 24.7%; Pred. No. 46;

Matches 37; Conservative 25; Mismatches 47; Indels 41; Gaps 9;

QY 3 GGAYGAGK-----AGGAFD-PYTLV-----RQPH---TILRVVSWLFSIVVFG 41

Db 383 GGSRGAGRLIIIIASMLSPFLPALIPLLKFSKSKMGPHKNSIYIVFSLGLLIIG 442

QY 42 SIWNEGYLNSAGEQFCIYNRNPACSYGAVGVLAFLTCLLYLALDYV----- 92

Db 443 --INMYFLSTSFVG--WLHNDLPKYAN--VLGAAVFPMLVYIVAVVYLTIRKDSVVT 496

QY 93 ----POISSVKDRKAVLSDIGV-SGEPHP 117

Db 497 FVADSSLAAVDAEKADAGDLAVDDDEPLP 526

RESULT 30

GCST\_CHICK

ID \_GCST\_CHICK STANDARD; PRT; 392 AA.

AC P28337;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine cleavage system T protein) (GCVT).

DE Name=AMT;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92406724; PubMed=1526969;

RA Okamura-Ikeda K., Fujiwara K., Motokawa Y.;

RT "Molecular cloning of a cDNA encoding chicken T-protein of the glycine cleavage system and expression of the functional protein in Escherichia coli. Effect of mRNA secondary structure in the translational initiation region on expression.";

RL J. Biol. Chem. 267:18284-18290(1992).

RN [2]

RP SEQUENCE OF 179-392 FROM N.A.

RP TISSUE=Liver;

RC MEDLINE=91161577; PubMed=2002038;

RX Okamura-Ikeda K., Fujiwara K., Yamamoto M., Hiraga K., Motokawa Y.;



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SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046866; AAH46866.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
DR SQ SEQUENCE 251 AA; 28297 MW; 436354C6D8330E21 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 251;
Best Local Similarity 23.5%; Pred. No. 47;
Matches 36; Conservative 23; Mismatches 46; Indels 48; Gaps 7;

QY 3 GGAYGAGKAGGADPVTYLR-----OPHTILRVVSMVLSIVVFGSIVN-----45
DB 5 GGLAGLGKK-----NPGAGLRWRLEPLGFKLLEWLFAPFGSCGSGSETAATVMCK 60

QY 46 -----ECYLSASEGQFCYNNRNPN--AC-----SYGVAVGVLAFL 80
DB 61 SEADTEIKLISVFPFYRLRYORYEMPACDDMERILHLTGDFSAFAPSFVMTGVAFL 120

QY 81 TCLLYLALDVYFPQISSVKDKKAVLSLDIGVSG 113
DB 121 YAMFALVILRPFHE-EYTKIRLPFIV-DLCVTG 151

RESULT 33
Q6ZM74 PRELIMINARY; PRT; 288 AA.
ID Q6ZM74
AC Q6ZM74;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE S1:zk70P6.6 (Novel protein similar to vertebrate synaptophysin (SYP))
DE (Fragment).
GN Names=syp; Synonyms=SI:zk70P6.6;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Beasley H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL831748; CAB50427.1; -.
DR ZFIN; ZDB-GENE-031104-2; syp.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 288 AA; 32151 MW; 186010E91045FB20 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 288;
Best Local Similarity 17.6%; Pred. No. 53;
Matches 23; Conservative 28; Mismatches 42; Indels 38; Gaps 4;

QY 18 YTLVRQHTILRVVSMVLSIVVF-----GSI-----VN 45
DB 7 FRLVKVPLGFKILEWFAIFAFSTCGSGSFRMSVECKNRSDNLKIDVDPEYPRFLH 66

SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046866; AAH46866.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 251 AA; 28297 MW; 436354C6D8330E21 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 439;
Best Local Similarity 22.1%; Pred. No. 81;
Matches 25; Conservative 30; Mismatches 44; Indels 14; Gaps 4;

QY 28 LRVSVMVLSIVV-----FGSIVNE-GYLNSASEGEQFCYNNRNPNACSYGVAVGV-----77
DB 289 MRMSFGVFWIAAGFAGVLRKTHGVESLVQTSIAHIGNNKKLAAPLMLVIGLVTMGI 348

QY 78 --AFLTCLLYLALDVYFPQISSVKDKKAVLSLDIGVSGEPHPAGTCTESTEG 128
DB 349 GSSFSF--IPILTTIFVPLCMQLGFSFPMATIIAGTAGALGDAGSPASDSTLG 399

RESULT 35
Q7NFW8 PRELIMINARY; PRT; 519 AA.
ID Q7NFW8
AC Q7NFW8;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE G113406 protein.
GN OrderedLocusNames=g113406;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Miyashita H., Tsuchiya T.,
RA Sasanoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RL DNA Reg. 10:137-145(2003).
DR EMBL: AF006580; BAC91347.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0008565; F:protein transporter activity; IEA.
DR GO: GO:0015031; P:protein transport; IEA.
DR InterPro: IPR010432; RDD.
DR InterPro: IPR006260; TonB_C.
DR Pfam: PF06271; RDD; 1.
DR TIGRFAMs: TIGR01352; tonB_Cterm; 1.
KW Complete proteome.
SQ SEQUENCE 519 AA; 54789 MW; 1756602E3FD37A8D CRC64;

Query Match 10.8%; Score 76; DB 2; Length 519;
Best Local Similarity 19.6%; Pred. No. 95;
Matches 30; Conservative 24; Mismatches 37; Indels 62; Gaps 4;

QY 31 VSWLFSIVVFGSIYNE-----GYLNSASGEQFCIYNR-----NPNACS----- 69
DB 132 VGVFDSVLFGLASGFLVLAFIFASLDGKGLDPKFANTRMIAADPRRTSANLYPAIV 191
QY 70 -----YGVAVGVLAFTLCILLYLALDVVFPQI----- 95
DB 192 SSILFIHLNVAANVLAIIPLFLALNIKFELTPEPPAPSWEFLLTDPDKVKPPEN 251
QY 96 -----SSVDRKKAVLSIDIGVSGEHPAGTP 121
DB 252 APKSNANSVAKNRQLPTDAGVKGAQPARPTP 284

RESULT 36
Q6TLGI PRELIMINARY; PRT; 232 AA.
ID Q6TLGI
AC Q6TLGI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaptophysin-like protein.
GN ORFNames=wu:fc22a07;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBF_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney marrow;
RA Song H.D., Chen Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY394944; AAQ94571.1; -.
DR ZFIN: ZDB-GENE-030131-2940; wu:fc22a07.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008021; C:synaptic vesicle; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR008253; Marvel.
DR InterPro: IPR001285; Synaptophysin.
DR Pfam: PF01284; MARVEL; 1.
DR PRINTS: PR00220; SYNAPTOPHYSIN.
SQ SEQUENCE 232 AA; 25806 MW; 1D55129BEEA9B9CA CRC64;

Query Match 10.7%; Score 75.5; DB 2; Length 232;
Best Local Similarity 25.2%; Pred. No. 48;

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Matches 29; Conservative 16; Mismatches 29; Indels 41; Gaps 4;
QY 21 VRQPTILRVVSWLFSIVVFG-----SIVNEG-----YLSNASE 54
DB 11 LKEPLGPIRVLEWIPAFATPGYSGSTSNFNVCKSSVTOEINASFSYFRLLTQSY 70
QY 55 GEQFCIYNR-----NPNACSYGAVGVLAFL-----TCLLYLALDVVFPQ 94
DB 71 KYPTCEANSTTFRTRQLTGDHSSAAEFFVAVGVLAFLYSTATLVLYGVQHLRYQ 125

RESULT 37
Y479 MYCTU
ID Y479 MYCTU STANDARD; PRT; 348 AA.
AC P64639; Q11145;
DT 01-OCT-1996 (Rel. 34, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Hypothetical protein Rv0479c/MT0497.
GN OrderedLocusNames=Rv0479c, MT0497; ORFNames=MTCV20G9.05c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBF_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekle A.F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
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CC
CC EMBL: EX842573; CAB00940.1; -.
DR EMBL: AE000516; AAK44720.1; -.
DR FIC: B70743; B70743.
DR TIGR: MT0497; -.
DR TubercuList: Rv0479c; -.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 111 131 Potential.
FT TRANSMEM 235 255 Potential.
SQ SEQUENCE 348 AA; 37048 MW; 9EBB7A8CF9E176C1 CRC64;

Query Match 10.7%; Score 75.5; DB 1; Length 348;

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Best Local Similarity 25.2%; Pred. No. 72;		Matches 40; Conservative 19; Mismatches 55; Indels 45; Gaps 7;	
QY	7	GAGKAGGADPYTLV-----RQPHILRVVSWLFSIVVFGSIVNVEGY- 48	
DB	76	GRQAHAQWDPDTGLLAAQEBAEPAVKTKRRARRDPLTVFLVLIIVFSLVLAGLIGGELYA 135	
QY	49	---LNSASEGEQFCIYNRNPNACSYGVAVGVLAFLTCLLYLALDVVFPQIS-----SVK 99	
DB	136	RHVANSKVAQAVCVVKDQATA-SFGVA-----PLLLMQVATRHFTNISVETAGNQIR 187	
QY	100	DRK----KAVLSDIGVSGEHPHAGT-----PCTESTEG 128	
DB	188	DAKGWQIKLTIONVRLKNTNSRGITGALDATTISSEG 226	
RESULT 38			
Y489_MYCBO			
ID	Y489 MYCBO	STANDARD; PRT; 348 AA.	
AC	P64700; Q11145;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DE	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Hypothetical protein Mb0489c.		
GN	OrderedLocusNames=Mb0489c;		
OS	Mycobacterium bovis.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.		
OX	NCBI_TaxID=1765;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AF2122/97;		
RX	MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;		
RA	Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,		
RA	Przyor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,		
RA	Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,		
RA	Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;		
RT	"The complete genome sequence of Mycobacterium bovis."		
RL	Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; BX248335; CAD93352.1; "		
KW	Complete proteome; Hypothetical protein; Transmembrane.		
FT	TRANSMEM 111 131 Potential.		
FT	TRANSMEM 235 255 Potential.		
SQ	SEQUENCE 348 AA; 37048 MW; 9EBB7A8CF9E176C1 CRC64;		
Query Match 10.7%; Score 75.5; DB 1; Length 348;			
Best Local Similarity 25.2%; Pred. No. 72;			
Matches 40; Conservative 19; Mismatches 55; Indels 45; Gaps 7;			
QY	7	GAGKAGGADPYTLV-----RQPHILRVVSWLFSIVVFGSIVNVEGY- 48	
DB	76	GRQAHAQWDPDTGLLAAQEBAEPAVKTKRRARRDPLTVFLVLIIVFSLVLAGLIGGELYA 135	
QY	49	---LNSASEGEQFCIYNRNPNACSYGVAVGVLAFLTCLLYLALDVVFPQIS-----SVK 99	
DB	136	RHVANSKVAQAVCVVKDQATA-SFGVA-----PLLLMQVATRHFTNISVETAGNQIR 187	
QY	100	DRK----KAVLSDIGVSGEHPHAGT-----PCTESTEG 128	
DB	188	DAKGWQIKLTIONVRLKNTNSRGITGALDATTISSEG 226	
RESULT 39			
Q6P2P0			
ID	Q6P2P0	PRELIMINARY; PRT; 460 AA.	
AC	Q6P2P0;		
DT	05-JUL-2004 (TRENBLrel. 27, Created)		
DT	05-JUL-2004 (TRENBLrel. 27, Last sequence update)		
DE	MATP protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Skin;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Skin;		
RA	Strausberg R.;		
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC064405; AAH64405.1; "		
SQ	SEQUENCE 460 AA; 51233 MW; 26901FD0438C14DD CRC64;		
Query Match 10.7%; Score 75.5; DB 2; Length 460;			
Best Local Similarity 28.7%; Pred. No. 94;			
Matches 29; Conservative 10; Mismatches 35; Indels 27; Gaps 4;			
QY	24	PH-----TILRVVSW-----LFSIVVFGSIVNVEGYLNSASEGEQFCIYNRNPNACSYGV 72	
DB	315	PHYRYLCISHLIGWTAFNLNMLFTDFMGQIVTRGDPYSAHNSTFLIYER-----GV 367	
QY	73	AVGVLAFLTCLLYLALDVVFPQISSVKDRKKAIVLSDIGVSG 113	
DB	368	EVGCWGFCSNVFSSLYSYF-----QKVLVSYIGLKG 399	
RESULT 40			
MATP_HUMAN			
ID	MATP_HUMAN	STANDARD; PRT; 530 AA.	
AC	Q3UMT9; Q9BTM3;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DE	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Membrane-associated transporter protein (AIM-1 protein) (Melanoma		
DE	antigen AIM1).		
GN	Name=MATP; Synonyms=AIM1;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM AIM-1A).		
RC	TISSUE=Melanoma;		
RX	MEDLINE=21115844; PubMed=11221837;		

RA Harada M., Li Y.F., El-Gamil M., Rosenberg S.A., Robbins P.F.;  
RT "Use of an in vitro immunoselected tumor line to identify shared  
RT melanoma antigens recognized by HLA-A\*0201-restricted T cells.";  
RL Cancer Res. 61:1089-1094(2001).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM AIM-1B).  
RX TISSUE=Skin;  
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins B.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zebrow B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP ALTERNATIVE SPLICING.  
RA Ferro S.;  
RL Unpublished observations (NOV-2001).  
RN [4]  
RP DISEASE, AND VARIANT LEU-374.  
RX MEDLINE=21473748; PubMed=11574907;  
RA Newton J.M., Cohen-Barak O., Hagiwara N., Gardner J.M., Davison M.T.,  
RA King R.A., Brilliant M.H.;  
RT "Mutations in the human orthologue of the mouse underwhite gene (uw)  
RT underlie a new form of oculocutaneous albinism, OCA4.";  
RL Am. J. Hum. Genet. 69:981-988(2001).  
CC -/- FUNCTION: Melanocyte differentiation antigen. May transport  
CC substances required for melanin biosynthesis (By similarity).  
CC -/- SUBCELLULAR LOCATION: Integral membrane protein; melanosome (By  
CC similarity).  
CC -/- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist;  
CC Name=AIM-1a;  
CC IsoId=O9UMX9-1; Sequence=Displayed;  
CC Name=AIM-1b;  
CC IsoId=O9UMX9-2; Sequence=VSP\_006297, VSP\_006298, VSP\_006299;  
CC Name=AIM-1c;  
CC IsoId=O9UMX9-3; Sequence=VSP\_006296;  
CC -/- TISSUE SPECIFICITY: Expressed in most melanoma cell lines and  
CC melanocytes.  
CC -/- DISEASE: Defects in MATP are the cause of oculocutaneous albinism  
CC type 4 (OCA4) [MIM:60574]. OCA4 is characterized by  
CC hypopigmentation of skin, hair and eyes. It leads to reduced  
CC visual acuity.  
CC -/- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)  
CC cation symporter transporter (TC 2.A.2) family.  
CC -/- CAUTION: Ref.2 sequence differs from that shown due to a  
CC frameshift in position 188.  
CC -/- CAUTION: The described alternatively spliced isoforms are inferred  
CC using information from ESTs.  
CC -/- DATABASE: NAME=Mutations of the MATP gene;  
CC NOTE=Retina International's Scientific Newsletter;  
CC WWW='http://www.retina-international.com/sci-news/matpmut.htm'.  
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CC -----  
DR EMBL; AF172849; AAD51812.1; -;  
DR EMBL; BC003597; AAH03597.1; ALT\_FRAME.  
DR GenBank; HGNC:16472; MATP.  
DR MIM; 606202; -;  
DR MIM; 606574; -;  
KW Albinism; Alternative splicing; Antigen; Glycoprotein;  
KW Melanin biosynthesis; Polymorphism; Transmembrane; Vision.  
FT DOMAIN 1 46 Cytoplasmic (Potential).  
FT TRANSMEM 47 67 Extracellular (Potential).  
FT DOMAIN 68 68 Extracellular (Potential).  
FT TRANSMEM 69 89 Extracellular (Potential).  
FT DOMAIN 90 110 Extracellular (Potential).  
FT TRANSMEM 111 131 Extracellular (Potential).  
FT DOMAIN 132 138 Extracellular (Potential).  
FT TRANSMEM 139 159 Extracellular (Potential).  
FT DOMAIN 160 184 Extracellular (Potential).  
FT TRANSMEM 185 205 Extracellular (Potential).  
FT DOMAIN 206 216 Extracellular (Potential).  
FT TRANSMEM 217 237 Extracellular (Potential).  
FT DOMAIN 238 318 Extracellular (Potential).  
FT TRANSMEM 319 339 Extracellular (Potential).  
FT DOMAIN 340 367 Extracellular (Potential).  
FT TRANSMEM 367 387 Extracellular (Potential).  
FT DOMAIN 388 398 Extracellular (Potential).  
FT TRANSMEM 399 419 Extracellular (Potential).  
FT DOMAIN 420 425 Extracellular (Potential).  
FT TRANSMEM 426 446 Extracellular (Potential).  
FT DOMAIN 447 477 Extracellular (Potential).  
FT TRANSMEM 478 498 Extracellular (Potential).  
FT DOMAIN 499 504 Extracellular (Potential).  
FT TRANSMEM 505 525 Extracellular (Potential).  
FT DOMAIN 526 530 Extracellular (Potential).  
FT CARBOHYD 356 356 N-linked (GlcNAc...) (Potential).  
FT VARSPLIC 129 187 Missing (in isoform AIM-1c).  
FT VARSPLIC 188 295 Missing (in isoform AIM-1b).  
FT VARSPLIC 386 406 Missing (in isoform AIM-1b).  
FT VARSPLIC 407 530 Missing (in isoform AIM-1b).  
FT VARIANT 374 374 F -> L.  
FT SEQUENCE 530 AA; 58301 MW; F14A4BACAA8FF31B CRC64;  
Query Match 10.7%; Score 75.5; DB 1; Length 530;  
Best Local Similarity 28.7%; Pred. No. 1.1e+02;  
Matches 29; Conservative 10; Mismatches 35; Indels 27; Gaps 4;  
QY 24 PH-----TILRVVSW-----LFSIVVFGSIVYNEGYLNSASEGEQFCIYRNPNACSYGV 72  
Db 315 PHRYLCISHLGWTAFSLNMLFFDTFMQIVYRGDPYSAHNSTEFLIVER-----GV 367  
QY 73 AVGVLAFLCLLYLALDVYFPQISSVKDRKKAVLSDIGVSG 113  
Db 368 EVGCGWGCINSVFSSLYSYF-----QKVLVSVIGLKG 399  
RESULT 41  
Q94614 PRELIMINARY; PRT; 249 AA.  
ID Q94614  
AC Q94614; Created  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
DE Alpha-expansion OSEXPAL8.  
GN Name=EXPA18;  
OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Erihartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21521099; PubMed=11641069; DOI=10.1016/S1369-5266(00)00211-9;  
 RA Lee X., Choi D., Kende H.;  
 RT "Expansins: ever-expanding numbers and functions.";  
 RL Curr. Opin. Plant Biol. 4:527-532(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22311554; PubMed=12428004; DOI=10.1104/pp.008888;  
 RA Lee X., Kende H.;  
 RT "Expression of alpha-expansin and expansin-like genes in deepwater rice.";  
 RL Plant Physiol. 130:1396-1405(2002).  
 CC -!- SIMILARITY: Belongs to the expansin family.  
 DR EMBL; AF394553; AAL24489.1; -.  
 DR Gramine; O94614; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.  
 DR InterPro; IPR009009; Barwin\_like.  
 DR InterPro; IPR002963; Expansin.  
 DR InterPro; IPR007112; Expan endogl.  
 DR InterPro; IPR007118; Expan Lol PI.  
 DR InterPro; IPR007117; Expan Lol PI C.  
 DR InterPro; IPR005132; Lipoprotein\_13.  
 DR Pfam; PF03330; DPBB 1; 1.  
 DR Pfam; PF01357; Pollen allerg 1; 1.  
 DR PRINTS; PR01226; EXPANSIN.  
 DR ProDom; PD002179; Expan Lol PI C; 1.  
 DR PROSITE; PSS0843; EXPANSIN\_CBD; 1.  
 DR PROSITE; PSS0842; EXPANSIN\_EG45; 1.  
 SQ SEQUENCE 249 AA; 26431 MW; B375CC995F08D650 CRC64;  
 Query Match 10.7%; Score 75; DB 2; Length 249;  
 Best Local Similarity 24.2%; Pred. No. 57;  
 Matches 23; Conservative 12; Mismatches 22; Indels 38; Gaps 3;  
 QY 3 GGAYGAGKAGGAFDPYTLVRQPHILRVSVWLSFVFGSIVNEGY-----LN 50  
 DB 32 GGADSGTGGAGC-----YGNLYDQGYGINNAALSTPLFNN 68  
 QY 51 SASGEQF---CIYNNPNACSVGVAVGLAFLTC 82  
 DB 69 GASCGQCYLIICNDYKAPSGCRMGTAITVTGTNFC 103  
 RESULT 43  
 Q635H8 PRELIMINARY; PRT; 439 AA.  
 AC Q635H8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Probable Na/H+ antiporter.  
 GN ORFNames=BTXK3859;  
 OS Bacillus cereus ZK.  
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=288681;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZK;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 RA Richardson P., Rubin E., Tice H.;  
 RT "Complete genome sequence of Bacillus cereus ZK";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CP000001; AAU16409.1; -.  
 SQ SEQUENCE 439 AA; 46439 MW; CBEB3FA565D24194 CRC64;  
 Query Match 10.7%; Score 75; DB 2; Length 439;  
 Best Local Similarity 22.1%; Pred. No. 1e+02;  
 Matches 25; Conservative 30; Mismatches 44; Indels 14; Gaps 4;  
 QY 28 LRVSVWLSFISW----FGSIVNE-GYINSASEGEQFCIYNNPNACSVGVAVGL----- 77  
 DB 289 MRWMSFGVWISNAGGAVLRKTGHVLSVQSAHIGNKPLAFLMLVIGLVTMGI 348  
 QY 78 --AFLTCLLYALDVPFQISVVKDKKAVLSIDIGVSGEPHPAGTCTESTEG 128  
 DB 349 GSSFST--IPILTIFVPLCQLGFSFPMATIAITAGALGDAGSPASDSTLG 399  
 RESULT 44  
 Q818Y3 PRELIMINARY; PRT; 439 AA.  
 ID Q818Y3;  
 AC Q818Y3;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Transport protein.  
 GN OrderedLocusNames=BC4103;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Erihartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21521099; PubMed=11641069; DOI=10.1016/S1369-5266(00)00211-9;  
 RA Lee X., Choi D., Kende H.;  
 RT "Expansins: ever-expanding numbers and functions.";  
 RL Curr. Opin. Plant Biol. 4:527-532(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22311554; PubMed=12428004; DOI=10.1104/pp.008888;  
 RA Lee X., Kende H.;  
 RT "Expression of alpha-expansin and expansin-like genes in deepwater rice.";  
 RL Plant Physiol. 130:1396-1405(2002).  
 CC -!- SIMILARITY: Belongs to the expansin family.  
 DR EMBL; AF394553; AAL24489.1; -.  
 DR Gramine; O94614; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.  
 DR InterPro; IPR009009; Barwin\_like.  
 DR InterPro; IPR002963; Expansin.  
 DR InterPro; IPR007112; Expan endogl.  
 DR InterPro; IPR007118; Expan Lol PI.  
 DR InterPro; IPR007117; Expan Lol PI C.  
 DR InterPro; IPR005132; Lipoprotein\_13.  
 DR Pfam; PF03330; DPBB 1; 1.  
 DR Pfam; PF01357; Pollen allerg 1; 1.  
 DR PRINTS; PR01226; EXPANSIN.  
 DR ProDom; PD002179; Expan Lol PI C; 1.  
 DR PROSITE; PSS0843; EXPANSIN\_CBD; 1.  
 DR PROSITE; PSS0842; EXPANSIN\_EG45; 1.  
 SQ SEQUENCE 249 AA; 26431 MW; B375CC995F08D650 CRC64;  
 Query Match 10.7%; Score 75; DB 2; Length 249;  
 Best Local Similarity 24.2%; Pred. No. 57;  
 Matches 23; Conservative 12; Mismatches 22; Indels 38; Gaps 3;  
 QY 3 GGAYGAGKAGGAFDPYTLVRQPHILRVSVWLSFVFGSIVNEGY-----LN 50  
 DB 32 GGADSGTGGAGC-----YGNLYDQGYGINNAALSTPLFNN 68  
 QY 51 SASGEQF---CIYNNPNACSVGVAVGLAFLTC 82  
 DB 69 GASCGQCYLIICNDYKAPSGCRMGTAITVTGTNFC 103  
 RESULT 43  
 Q635H8 PRELIMINARY; PRT; 439 AA.  
 AC Q635H8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Probable Na/H+ antiporter.  
 GN ORFNames=BTXK3859;  
 OS Bacillus cereus ZK.  
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=288681;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZK;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 RA Richardson P., Rubin E., Tice H.;  
 RT "Complete genome sequence of Bacillus cereus ZK";  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CP000001; AAU16409.1; -.  
 SQ SEQUENCE 439 AA; 46439 MW; CBEB3FA565D24194 CRC64;  
 Query Match 10.7%; Score 75; DB 2; Length 439;  
 Best Local Similarity 22.1%; Pred. No. 1e+02;  
 Matches 25; Conservative 30; Mismatches 44; Indels 14; Gaps 4;  
 QY 28 LRVSVWLSFISW----FGSIVNE-GYINSASEGEQFCIYNNPNACSVGVAVGL----- 77  
 DB 289 MRWMSFGVWISNAGGAVLRKTGHVLSVQSAHIGNKPLAFLMLVIGLVTMGI 348  
 QY 78 --AFLTCLLYALDVPFQISVVKDKKAVLSIDIGVSGEPHPAGTCTESTEG 128  
 DB 349 GSSFST--IPILTIFVPLCQLGFSFPMATIAITAGALGDAGSPASDSTLG 399  
 RESULT 44  
 Q818Y3 PRELIMINARY; PRT; 439 AA.  
 ID Q818Y3;  
 AC Q818Y3;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Transport protein.  
 GN OrderedLocusNames=BC4103;





RX PubMed=14960714; DOI=10.1093/nar/gkh258;  
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,  
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,  
RA Nelson W.C., Koistoe A.-B., Fraser C.M., Read T.D.;  
RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic  
adaptations and a large plasmid related to *Bacillus anthracis* pX01."  
RL Nucleic Acids Res. 32:977-988(2004).  
DR EMBL; AE017264; AAS38989.1; -;  
DR TIGR; BCE0053; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.  
DR InterPro; IPR002797; Polysacc synt.  
DR Pfam; PF01943; Polysacc synt; 1.  
KW Complete proteome.  
SQ SEQUENCE 533 AA; 58652 MW; D652376B752A1019 CRC64;  
  
Query Match 10.6%; Score 74.5; DB 2; Length 533;  
Best Local Similarity 20.4%; Pred. No. 1.4e+02;  
Matches 22; Conservative 24; Mismatches 33; Indels 29; Gaps 4;  
  
QY 27 ILRVSWLFSIVVFGSIYN---EGVLN-----SASE-----GEQFCI 60  
Db 125 LURVISFSFILPFLSVARGYQGFNNMPTAVSQVIEQTIRVSIIVFLSLFLIAHEFDL 184  
  
QY 61 YNRNPNCAGYGVAGVLAFLTCLLYALD---VYRPQISSVKDRKAV 105  
Db 185 YTVGAGMLGSIAGGLIGIIVILYMRHDFRSIFFKSVKRIKGGKII 232  
  
RESULT 50  
Q81VY5 PRELIMINARY; PRT; 533 AA.  
AC Q81VY5; Q6I4Y9; Q8KYN3;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Stage V sporulation protein B, putative.  
GN OrderedLocusNames=BA0054, BAS0054, GBAA0054;  
OS *Bacillus anthracis*.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
OX NCBI\_TaxID=1392;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ames / isolate Porton;  
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;  
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,  
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,  
RA Holtzapple E.K., Oekstad O.A., Helgason E., Rillstone J., Wu M.,  
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,  
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
RA Hazen A., Cline R.T., Redmond C., Thwaites J.E., White O.,  
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,  
RA Hanna P.C., Koistoe A.-B., Fraser C.M.;  
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to  
closely related bacteria."  
RL Nature 423:81-86(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ames / isolate 0581;  
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,  
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,  
RA Fraser C.M.;  
RT "Bacillus anthracis comparative genomics."  
RL Submitted (May-2004) to the EMBL/GenBank/DBAJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sterner;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBAJ databases.  
DR EMBL; AE017024; AAP24109.1; -;  
DR EMBL; AE017334; AAT29132.1; -;  
DR EMBL; AE017225; AAT52392.1; -;  
DR TIGR; BAA0054; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.  
DR InterPro; IPR002797; Polysacc synt.  
DR Pfam; PF01943; Polysacc synt; 1.  
KW Complete proteome.  
SQ SEQUENCE 533 AA; 58670 MW; 99FC61F7815F81AE CRC64;  
  
Query Match 10.6%; Score 74.5; DB 2; Length 533;  
Best Local Similarity 20.4%; Pred. No. 1.4e+02;  
Matches 22; Conservative 24; Mismatches 33; Indels 29; Gaps 4;  
  
QY 27 ILRVSWLFSIVVFGSIYN---EGVLN-----SASE-----GEQFCI 60  
Db 125 LURVISFSFILPFLSVARGYQGFNNMPTAVSQVIEQTIRVSIIVFLSLFLIAHEFDL 184  
  
QY 61 YNRNPNCAGYGVAGVLAFLTCLLYALD---VYRPQISSVKDRKAV 105  
Db 185 YTVGAGMLGSIAGGLIGIIVILYMRHDFRSIFFKSVKRIKGGKII 232  
  
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